

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 17, 2002, 19:19:10 ; Search time 61.73 Seconds

(without alignments)
759.325 Million cell updates/sec

Title: US-09-765-068-2

Perfect score: 2248

Sequence: 1 MDHPREDEHQRTTKPMAQ.....EAKCCFFKRRKKTQAKRK 422

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A.GeneSeq_032802:*

- 1: /SIDSL/gcgdata/geneSeq/geneSeq-emb1/AA1980.DAT:*
- 2: /SIDSL/gcgdata/geneSeq/geneSeq-emb1/AA1981.DAT:*
- 3: /SIDSL/gcgdata/geneSeq/geneSeq-emb1/AA1982.DAT:*
- 4: /SIDSL/gcgdata/geneSeq/geneSeq-emb1/AA1983.DAT:*
- 5: /SIDSL/gcgdata/geneSeq/geneSeq-emb1/AA1984.DAT:*
- 6: /SIDSL/gcgdata/geneSeq/geneSeq-emb1/AA1985.DAT:*
- 7: /SIDSL/gcgdata/geneSeq/geneSeq-emb1/AA1986.DAT:*
- 8: /SIDSL/gcgdata/geneSeq/geneSeq-emb1/AA1987.DAT:*
- 9: /SIDSL/gcgdata/geneSeq/geneSeq-emb1/AA1988.DAT:*
- 10: /SIDSL/gcgdata/geneSeq/geneSeq-emb1/AA1989.DAT:*
- 11: /SIDSL/gcgdata/geneSeq/geneSeq-emb1/AA1990.DAT:*
- 12: /SIDSL/gcgdata/geneSeq/geneSeq-emb1/AA1991.DAT:*
- 13: /SIDSL/gcgdata/geneSeq/geneSeq-emb1/AA1992.DAT:*
- 14: /SIDSL/gcgdata/geneSeq/geneSeq-emb1/AA1993.DAT:*
- 15: /SIDSL/gcgdata/geneSeq/geneSeq-emb1/AA1994.DAT:*
- 16: /SIDSL/gcgdata/geneSeq/geneSeq-emb1/AA1995.DAT:*
- 17: /SIDSL/gcgdata/geneSeq/geneSeq-emb1/AA1996.DAT:*
- 18: /SIDSL/gcgdata/geneSeq/geneSeq-emb1/AA1997.DAT:*
- 19: /SIDSL/gcgdata/geneSeq/geneSeq-emb1/AA1998.DAT:*
- 20: /SIDSL/gcgdata/geneSeq/geneSeq-emb1/AA2000.DAT:*
- 21: /SIDSL/gcgdata/geneSeq/geneSeq-emb1/AA2001.DAT:*
- 22: /SIDSL/gcgdata/geneSeq/geneSeq-emb1/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2248	100.0	422	22	AAG67392
2	2248	100.0	422	22	AAU04636
3	2219.5	98.7	459	22	AAG67542
4	2157	96.0	438	22	AAB97904
5	1669.5	74.3	377	15	AAB97529
6	1669.5	74.3	377	16	AAR76625
7	1571.5	69.9	347	15	AAR56530
8	1571.5	69.9	347	16	AAR76626
9	1553	69.1	422	22	AAB66550
10	1553	69.1	422	22	AAB71525
11	942.5	41.9	416	21	AAV90264

12	938	41.7	476	21	AAG45046	Arabidopsis thalia
13	936	41.6	415	15	AAR56531	Protein kinase (CK
14	936	41.6	415	16	AAR76627	Human HRR25-like c
15	933	41.5	468	21	AAG45810	Arabidopsis thalia
16	930	41.4	475	21	AAG41798	Arabidopsis thalia
17	930	41.4	475	21	AAG46931	Arabidopsis thalia
18	930	41.4	479	21	AAG41797	Arabidopsis thalia
19	930	41.4	479	21	AAG46930	Arabidopsis thalia
20	927	41.2	471	21	AAG31488	Arabidopsis thalia
21	927	41.2	471	21	AAG39489	Arabidopsis thalia
22	924	41.1	365	15	AAR56520	Protein kinase (Hh
23	924	41.1	365	16	AAR76616	Schizosaccharomyce
24	921	41.0	321	21	AAG30651	Arabidopsis thalia
25	918.5	40.9	450	21	AAG31130	Arabidopsis thalia
26	918	40.8	451	21	AAG30687	Arabidopsis thalia
27	918	40.8	457	21	AAG30686	Arabidopsis thalia
28	907.5	40.4	400	15	AAR56521	Protein kinase (Hh
29	907.5	40.4	400	16	AAR76617	Schizosaccharomyce
30	903.5	40.2	474	22	AAU00538	Maize casein kinas
31	900	39.9	475	21	AAG39947	Arabidopsis thalia
32	897.5	39.9	433	21	AAG09277	Arabidopsis thalia
33	897.5	39.9	433	21	AAG43458	Arabidopsis thalia
34	890.5	39.6	435	21	AAG39733	Arabidopsis thalia
35	885	39.4	440	22	AAB58733	Drosophila melanog
36	885	39.4	440	22	AAB67179	Drosophila melanog
37	885	39.4	440	22	AAB67180	Drosophila melanog
38	884	39.3	440	21	AAB01923	Wild-type Drosophi
39	880	39.1	440	21	AAB01925	Mutant Drosophila
40	876	39.0	440	21	AAB01924	Mutant Drosophila
41	862.5	38.4	335	15	AAR56522	Protein kinase (CK
42	862.5	38.4	337	16	AAR76618	Human HRR25-like c
43	862.5	38.4	337	15	AAR56524	Protein kinase (CK
44	862.5	38.4	337	16	AAR76620	Human HRR25-like c
45	862.5	38.4	332	21	AAR56608	Human prostate can

ALIGNMENTS

RESULT	1
AA67392	standard; Protein: 422 AA.
XX	AA67392:
AC	AA67392:
XX	13-NOV-2001 (first entry)
DE	Amino acid sequence of human protein kinase SGK248.
XX	Human; protein kinase; cancer; immune disease; cardiovascular disease;
KW	brain disease; neuronal disease; Alzheimer's disease; chromosome 3;
KW	Parkinson's disease; multiple sclerosis; metabolic disorder;
KW	peripheral nervous system disease; amyotrophic lateral sclerosis;
KW	infection; ocular disease; migraine; pain; sexual dysfunction;
KW	mood disorder; attention disorder; cognition disorder; hypertension;
KW	hypertension; psychotic disorder; dyskinesia; transplant rejection.
XX	
OS	Homo sapiens.
XX	
PN	WO200166594-A2.
XX	
PD	13-SEP-2001.
XX	
PF	02-MAR-2001; 2001MO-US06838.
XX	
PR	06-MAR-2000; 2000US-0187150.
XX	
PR	29-MAR-2000; 2000US-0193404.
XX	
PR	13-NOV-2000; 2000US-0247013.
XX	
PA	(SUGEN) SUGEN INC.
XX	
PI	Plowman GD, Whyte D, Manning G, Sudarsanam S, Martinez R;
XX	

DR	WPI: 2001-536777/59.
DR	N-PSDB: AAH71991.
XX	
PT	Nucleic acids capable of encoding human polypeptides having a kinase or
PT	kinase-like activity, useful for diagnosing a disease selected from
PT	cancers, cardiovascular disease and neuronal-associated diseases (e.g.
PT	Alzheimer's disease) -
XX	
PS	Claim 7, Fig 2A: 201pp: English.
XX	
CC	The present sequence represents a human protein kinase. The
CC	gene is located at chromosomal position 3p24.2-p21.3. The kinase
CC	polypeptides are useful for diagnosing a disease or disorder
CC	selected from cancers (e.g. cancers of tissues and cancers of
CC	hematopoietic origin), immune-related diseases and disorders,
CC	cardiovascular disease, brain or neuronal-associated diseases (e.g.
CC	Alzheimer's disease, Parkinson's disease, multiple sclerosis),
CC	metabolic disorders, peripheral nervous system diseases, amyotrophic
CC	lateral sclerosis, viral infections, infections caused by prions,
CC	infections caused by bacteria, infections caused by fungi, ocular
CC	diseases, migraines, pain, sexual dysfunction, mood disorders,
CC	attention disorders, cognition disorders, hypotension, hypertension,
CC	psychotic disorders, dyskinesias, and organ transplant rejection.
CC	kinase inhibitors are useful for treating diseases and disorders
CC	described above.
XX	
XX	
XX	
Sequence	422 AA;
2Q	

Query Match	100.0%;	Score 2248;	DB 22;	Length 422;
Best Local Similarity	100.0%;	Pred. No. 5.7e-231;		
Matches 422;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY 1 MDHRSREDDERQPTTKPAORSAICSPSPSGSSSSGVLAMGPNFRVAKTKIGCGNGFGLRL 60
Db 1 mdhsrrekdqrlltkpmaqrshahcspspssssgyllmvgpnfrvgkklgcygnfgllrl 60
QY 61 GKNTYNTNEYAIKLEPIKSRAPQLHLEKRYKQLGSGAGBGLPOVYYFGPGCGKIYAMVLEL 120
Db 61 gknltyntneyaivkilepiksrpqqlhleyryfkqgssagsglpqvyyfpgpgcknyamvlel 120

Qy	121	LGPSIEDLEDCDRFTFLKTVIMIAIOLLSRMEVYHSKULIYRDVYPENELIGROGNKE	1800
Db	121	lpsledlfdcdrtflktvimaiaqlslrmevshskuliyrdvypenfligrqgnke	1800

OY	181 HVHIDFGGLAKKEYIDPETKKHIPIYREHKSLTGTARWYSINTHLGKQOSRRDDLEALGHM 240
Dd	181 hvhiidfglakeyidpetkkihpiyrehkstlgtarwysintthlgkqosrrddlealgym 240

QY 241 FMVILRGSLPWQGLKADTLKERYQKIGDTKRNPPIEALCENFPEEMATYLRVYRRLDFFE 3000
 |||||
 Db 241 fmvilrgslpwqglkadtlkeryqkigdtkrnppiealcenfpematyrvyrrldffe 3000

QY 301 KPDVEYLRTLEFTDLEFEKGYTFDYAYDVGRIPTPVGSVHVDSGASAITRESHTHRDRP 360

361 SQQPPLRNQVSSITNGELNVDPTGAHSNAPITAAHAEVVEEAKKCCFFKRRKRTAQR 4200

DB	301	sqgqplrnqyvssrngelnvaoqpcgansnapilanaeveveeakcccllrlrlrlklclqr	420
QY	421	HK 422	
	11		

Db 421 hK 422

RESULT 2

AAU04636
ID AAU04636 standard; Protein; 422 AA.
XX
AC AAU04636;

XX 26-SEP-2001 (first entry)
DT

XX Human kinase protein.

Human; kinase protein; hybridisation probe; therapeutic; gene therapy;
antisense-therapy; drug screening.

XX
OS
XX

Homo sapiens

PN W0200153493-A2.

XX 26-JUL-2001.
PD
XX

18-JAN-2001; 2001WO-US02120.

AA 18-JAN-2000; 2000US-0176690.
PR
YY

AA
PA
XY
(LEXI-) LEXICON GENETICS INC.

AA Donoho G, Hilbun E, Turner CA, Friedrich G, Zambrowicz B,
PI
PI
PI Sands AM, PI

FI SAUCS RI,
XX
DB WBT: 2001-443260/47

DR WFI, 2001-44220V/7/

Abstract An isolated nucleic acid molecule encoding a novel human protein useful as a therapeutic and to screen libraries isolate clones and prepare

us libraries and to screen libraries for
cloning and sequencing templates -

aa Claim 2; Page 31-32; 33pp; English.
ps
xy

CC The sequence represents the amino acid sequence of a novel human kinase
CC protein. The nucleic acid sequence can be used to screen libraries,
CC isolate clones and prepare cloning and sequencing templates and as
CC hybridisation probes for screening libraries, and as therapeutics such
CC as antisense-therapy and gene-therapy. Probes derived from the DNA
CC or polypeptide sequences can be used in the identification, selection
CC and validation of novel molecular targets for drug discovery.

XX	Sequence	422 AA;
SQ		

Query Match	100.0%	Score 2248;	DB 22;	Length 422;
Best Local Similarity	100.0%;	Pred. No. 5.7e-231;		
Matches 422;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Q7 1 MDHSREKDEPQRTTKPAAQSAHCSRPSSSSSGVLTAMGPNPRVGKIGCNFGLRL 60
|||||
Db 1 mdhpsrekdeqrttkpmaqsahcsrpsgssasylmvgnprvgkikigcngfelrl 60

QY 61 GKNITYNEYYAIKLEPIKSRAPOLHLEYRYFKOLGSAGEGLPOVYFFGPCGKYNNAMYLEL 120
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 61 gknlytneyyaaiklepksrapqhlleyryfkyqgsagcglppvyffgpcgkynnamylel 120

Oy 121 LGSLEEDLFDICDRFTTLKTVIMAIQDLSRMEVYHSKULIYRDYKPENFLIGROCNKE 180
 |||||
Db 121 lgspledlfdicdrfttlktvimaiaqlismeyvshskuliyrdykpenfligrqnke 180

QY 181 HVIIHIDFGLAEYIDETKKAIPYREHKSLSLTGARVMSINTHLGKQOSRRDDLALGIM 240
|||||
189 hvvvtvtdffclakewvthetkthnvrelkslfrayvmsintvhlqkqstrddlcaatqhm 240
|||||

241 FMYLRGSLWQGLKADTLKERYOKIGDTKRNPPIALCENFPPEEMATYLRVYRLDFFE 300

Db 241 tmylrlgsdpmgglkacdlkerygkigatckinfpiaeatcenipbeamaLytllyvritiore 300

QY 301 KPDVEYLRLTFTDLFEKKGYTEPDYADWNGRPITPVGSVHVDGASAIPTRESHTHRDP 360

[illegible]

00 301 sqqprlnqvssrlgetlrvudpcrgansuafricandevceveearccclnnnnnnnncfda 72

QY 421 HK 422
II
Db 421 hk 422

RESULT 3

AAG67542

ID AAG67542 standard; Protein; 459 AA.

XX AAG67542;

XX 26-NOV-2001 (first entry)

XX Amino acid sequence of human kinase 15977.

XX Human; kinase; 2504; 15977; 14760; cellular proliferative disorder;
XX cellular differentiative disorder; neural disorder; immune disorder;
XX cardiovascular disorder; liver disorder; skin disorder;
XX skeletal muscle disorder; bone metabolism; cardiovascular disorder;
XX viral disease; pain; metabolic disorder; blood vessel disorder;
XX hepatic disorder; liver disorder.

XX Homo sapiens.

Location/Qualifiers

FT Modified-site 14..16 /note- "predicted protein kinase C phosphorylation site"

FT Domain 44..329 /note- "serine/threonine kinase domain"

FT Domain 44..276 /note- "eukaryotic protein kinase domain"

FT Modified-site 96..99 /note- "predicted casein kinase II phosphorylation site"

FT Modified-site 124..127 /note- "predicted casein kinase II phosphorylation site"

FT Modified-site 137..139 /note- "predicted protein kinase C phosphorylation site"

FT Modified-site 150..153 /note- "predicted casein kinase II phosphorylation site"

FT Modified-site 199..201 /note- "predicted protein kinase C phosphorylation site"

FT Modified-site 214..216 /note- "predicted protein kinase C phosphorylation site"

FT Modified-site 229..231 /note- "predicted protein kinase C phosphorylation site"

FT Modified-site 229..232 /note- "predicted casein kinase II phosphorylation site"

FT Modified-site 258..260 /note- "predicted protein kinase C phosphorylation site"

FT Modified-site 258..261 /note- "predicted casein kinase II phosphorylation site"

FT Modified-site 269..271 /note- "predicted casein kinase II phosphorylation site"

FT Modified-site 270..273 /note- "predicted protein kinase C phosphorylation site"

FT Modified-site 273..276 /note- "predicted CAMP- and cAMP-dependent protein kinase phosphorylation site"

FT Modified-site 355..357 /note- "predicted casein kinase II phosphorylation site"

FT Modified-site 355..358 /note- "predicted protein kinase C phosphorylation site"

FT Modified-site 370..373 /note- "predicted casein kinase II phosphorylation site"

FT Modified-site 373..375 /note- "predicted N-glycosylation site"

FT Modified-site 388..391 /note- "predicted protein kinase C phosphorylation site"

FT Modified-site 411..414 /note- "predicted N-glycosylation site"

FT Modified-site 451..454 /note- "predicted casein kinase II phosphorylation site"

FT Modified-site /note- "predicted CAMP- and cAMP-dependent protein kinase phosphorylation site"

FT Modified-site 422..427
FT /note- "predicted N-myristoylation site"
FT Modified-site 46..49
FT /note- "predicted amidation site"

XX WO200164905-A2.

XX 07-SEP-2001.

XX 28-FEB-2001; 2001WO-US06525.

XX 29-FEB-2000; 2000US-0186061.

XX (MILL-) MILLENNIUM PHARM INC.

XX Olandt PJ, Kapeller-Libermann R, Meyers RA;

XX WPI; 2001-570697/64.

XX New protein kinase family polypeptides for treating hematopoietic

XX neoplastic disorders, immune disorders, cardiovascular disorders and

XX disorders of blood vessels

XX Claim 8; Fig 4A-C; 145pp; English.

XX The present sequence represents human kinase 15977. The specification

XX also describes kinases 2504 and 14760. The kinase polypeptides and

XX polynucleotides are used to treat cellular proliferative or

XX differentiative disorders, neural disorders, immune disorders,

XX cardiovascular disorders, liver disorders, skin disorders and skeletal

XX muscle disorders. They may also be used for controlling disorders

XX associated with bone metabolism, cardiovascular disorders, viral

XX diseases, pain or metabolic disorders, blood vessel

XX disorders, and hepatic or liver disorders.

XX Sequence 459 AA:

Query Match 98.7%; Score 2219.5; DB 22; Length 459;

Best Local Similarity 91.9%; Pred. No. 7.2e-228; Matches 422; Conservative 0; Mismatches 0; Indels 37; Gaps 1;

QY 1 MDHPSREKDERQRTTKPMAQSAHCSRPSSSSSGVLMVGNPFRVKKIGCNFGEIQL 60
DB 1 mdhpsrkedergtrtkpmagsahcsrpsgssssgvlmvgnpfrvkkigcgnfigelrl 60
QY 61 GKNLYTNEYVAIKLEPIKSAPOHLLEYRFYKQLGSAEGLPQVYIFGPGCKYAMVLEL 120
DB 61 gknlytneyvaiklepiksapohlleyrfykqlgsageglpqvyifgpcgkyamvlel 120
QY 121 LQPSLEDLPFLCDRTFLTKVYLMATIDLSRMEVYHKNLIRVKNENPLIGRGNKKE 180
DB 121 lqpsledlflcdrtfltkvylmatidlsrmevynhknliyrvknennpligrgnkke 180
QY 181 HVHIIDFGLAKEVIDEPTKKHPIPYREHKSITGFAVRSINTHLGKQSRDDEALGIM 240
DB 181 hvhiidfglakevidetpkkhpiyrehsitgfarvrsinthlgkqsrddelalgim 240
QY 241 FMYELRGLSPWGLKADTLKERYOKIDTRKNTPIEALCENFPEMATYLRVYRLDFFE 300
DB 241 fmyelrglspwglkadtlkeryokidtrkntpiealcenfpemategyrvrldffe 300
QY 301 KPDEYIIRTLFTDLFEKKGITFDYAYRWGRRPTPYGSVHVDSGASATIRSHTHDRP 360
DB 301 kpdeyirrtlftdlfekkgitfdyayrwgrrptpygsvhvdsagasatirshthdrp 360
QY 361 SQOQPLRN-----QVSSSTNGELANVDP 383
DB 361 sqoqplrnqnvsserrgweilpsrqtntsylltslaadhgsavqvssstngelnvddp 420
QY 384 TGAHNSAPIFAHAEEVEVEEAKCCCFEKKRRKRTAQRHK 422
DB 421 tgaahnsapifahaeeveveeakcccfekrrkrktaqghk 459

RESULT 4
ID AAB97904 standard; Protein: 438 AA.
XX
AC AAB97904;
XX
DT 10-AUG-2001 (first entry)
XX
DE Human casein kinase 48 protein SEQ ID NO:2.
XX
KW Human: casein kinase 48; cytosolic; immunomodulatory; antiinflammatory;
KW vitruicide; gene therapy; diagnosis; treatment; malignant tumour;
KW haemopathy; HIV infection; immunological disease; inflammation.
XX
OS Homo sapiens.
XX
PN WO200129228-A1.
XX
PD 26-APR-2001.
XX
PF 16-OCT-2000; 2000WO-CN00330.
XX
PR 18-OCT-1999; 99CN-0116987.
XX
PA (SHAN-) SHANGHAI BIO ROAD GENE DEV LTD.
XX
PI Mac Y, Xie Y;
XX
DR WPI: 2001-282163/29.
DR N-PSDB: AAH21501.
XX
PT Human casein kinase 48 and encoded polynucleotide, applicable in
PT diagnosis and treatment of malignant tumor, hemopathy, HIV infection,
PT immunological diseases and various inflammation -
XX
PS Claim 1; Page 23-24; 30pp; Chinese.
XX
CC The present sequence represents human casein kinase 48 (CK48). CK48 has
CC cytosolic, immunomodulatory, antiinflammatory and vitruicide activity,
CC and can be used in gene therapy. The CK48 protein and polynucleotide
CC sequences can be used in the diagnosis and treatment of malignant
CC tumour, haemopathy, HIV infection, immunological diseases and various
CC inflammation.
XX
SQ Sequence 438 AA;
XX
Query Match 96.0%; Score 2157; DB 22; Length 438;
Best Local Similarity 99.0%; Pred. No. 3.2e-221;
Matches 407; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
OY 1 MDHRSREKDERQRTTKPAORSAHCSRRSSSSGVLAVGPNFVRGKKIGCGNGEIRL 60
Db 1 mdhpsrekdqrctkpmagrsahcstrpssssgvilmvgnrtfvgkklcgnfgeirl 60
OY 61 GKNLYTNEYVAIKLEPIKSRAPOLHLEYRKYKOLGAGEGLPOVYFFGCGKNMAYEL 120
Db 61 gknlytneyvaiklepiksrappqlhleyrfykqigsageglpvyvffpcgkynamvel 120
OY 121 LGSFLEDFLDCDRFTITKTYLMLAIQLLSRMEYVHSKNLIYRDYKPNFLIGRGNKE 180
Db 121 lgsfledfldcdrtfcltkvmlaqlllsrmevhsknliyrdivkpenfligrgnke 180
OY 181 HVHIDHGLAKETIDPETKHIPREKSLTGTARYSINTMHLGKEQSRDDLEALGHM 240
Db 181 hvhldhglakeyidpetkhipreksltgtarymsintmhlgkesrddlealghm 240
OY 241 FMYFLRGSIPWQGLKADTLKERYOKIGDTKRNTPLEALCENFPEEMATYLRVYRLDFE 300
Db 241 fmyflrsgslpwqglkadtlkerykigdtktrntplealcenfpematylyrvrldffe 300

OY 301 KPDYELRLTFLDLEFKKGYTFDYAVDWGRRPIPTPVGSVVDGASATRESHTHRDP 360
Db 301 kpdyeylrlltflldlefkkytfdyavdwgrrpipygsvvndgsatlreshtdrp 360
OY 361 SQOOPLRNQVVSSTNGELNVDDPTGAHSNAPITAAEVEVEAEACCCFFK 411
Db 361 sqqoplrnqvvsstngelnvddptgahsnapitaaevveeakclmfhk 411
RESULT 5
ID AAR56529 standard; Protein: 377 AA.
XX
AC AAR56529;
XX
DT 17-MAR-1995 (first entry)
XX
DE Protein kinase (CKigamma1Hu).
XX
KW Protein kinase; immunogen; antibody; protein-tyrosine kinase;
KW protein-serine/threonine kinase; recombination; repair; screening;
KW detection; casein kinase.
XX
OS Homo sapiens.
XX
PN WO9417189-A.
XX
PD 04-AUG-1994.
XX
PF 21-JAN-1994; 94WO-US00795.
XX
PR 21-JAN-1993; 93US-0008001.
XX
PA (SALK) SALK INST BIOLOGICAL STUDIES.
XX
PI Hoekstra MF;
XX
DR WPI: 1994-264102/32.
DR N-PSDB: AAO56529.
XX
PT Wild-type and mutant protein kinase genes and encoded
PT polypeptide(s) - Useful in screening for compositions which may
PT effect DNA double strand break repair activity
XX
PS Claim 11; Page 100-101; 121pp; English.
XX
CC This sequence is a protein kinase similar to the HRR25 protein of
CC Saccharomyces cerevisiae which is described in AAR56519.
CC Host cells stably transformed with the protein kinase encoding DNA
CC may be used for the expression of the protein kinase such that the
CC expressed protein is "displayed" on the host cell surface. The
CC cells may then be used as immunogen for the production of antibodies.
CC The host cells may also be used for the large scale production of the
CC protein kinase, the expressed protein being either isolated from the
CC cell surface or from the culture medium. Recombinant HRR25 like
CC proteins display a number of properties which are unique among the
CC eukaryotic protein kinases e.g. the HRR25 protein possesses both
CC protein-tyrosine kinase and protein-serine/threonine kinase
CC activities. Also, HRR25 operates to promote repair of DNA strand
CC breaks at a specific nucleotide sequence and is the only protein
CC kinase known to have such recombination/repair promoting activity.
CC Recombinant HRR25-like proteins and host cells expressing them are
CC useful in screening methods designed to examine the effects of
CC various compositions on DNA break repair and protein kinase
CC activities of the protein. The HRR25-like proteins are casein
CC kinase class I protein kinases.
XX
SQ Sequence 377 AA;
XX
Query Match 74.3%; Score 1669.5; DB 15; Length 377;
Best Local Similarity 84.8%; Pred. No. 3e-169;
Matches 318; Conservative 21; Mismatches 27; Indels 9; Gaps 5;

Oy	21	RSASRSPSSGSSSSGVLMVPPNFRVGKKICGNFGEIATGKNTYTNEYVAKLEPIKSR	80
Db	7	rsghntrtctg-ssssgvltmvgpnrtivgkklgcnfgeltrgknltyneyvaklepnksr	65
Oy	81	APQHLREYRFYKQDSAGEGLSPQVYTFGPGCKYNAWVLELGPSELDLPDLCRTFTLKT	140
Db	66	apqhlleyrf/ykqjgs-9dglpvyuyfsgpcgkyamwvlellgpelldlfdlcldrftalc	124
Oy	141	VIMATVQLSSMEVYHSSKNLYRQVKNRKNENFLIGQSKKKEVYHIIIDFGIAKEYIDETK	200
Db	125	vimalqqlstsmeyvhsnknllyrvkvkenflfgrpnkltqgvhlldfglakeyidpeck	184
Oy	201	KHIPPREEKSLTGTARYKSYINTHNGKQSRRDDLEALGHHMFYELRSGSLPMQGIKADTLK	260
Db	185	khpprekhsltgcaryksintthngkqsrddlealghmfyelyrsgslpmqgikadtlk	244
Oy	261	ERYQKIGDTKNTPELIALCENFPEEMATYLYRYRRLDFFEKRPDEYLRTLFTLDFEKKGY	320
Db	245	eryqkigtckrtatplevlceafpeemattlyrvrldffekrpdelylrkltfdlfdarkgy	304
Oy	321	TFDPAVDMVGRPIPTPGSVYHVDGSAATIRRSTHTRDSQQQPLRNOVVSSTNGELNY	380
Db	305	mfdeydwlgvqltctpygaavgqdpals-nreaqhldkmgqs---knqvssstngelnlt	360
Oy	381	DDPTG---AHSNAPI 392	
Db	361	ddptadvgmhpsqpl 375	
RESULT	6		
ID	AAR76625		
XX	AAR76625 standard; Protein; 377 AA.		
AC	AAR76625;		
XX			
DT	25-JAN-1996 (first entry)		
XX			
DE	Human HRR25-like casein-kinase-I CK1-gamma-1Hu protein.		
XX			
KW	Casein-kinase-I, HRR25; protein-tyrosine-kinase; CK1-gamma-1Hu;		
KW	Protein-serine/threonine-kinase; enzyme; DNA repair;		
KW	DNA recombination.		
XX			
OS	Homo sapiens.		
XX			
PN	MO9519993-A1.		
XX			
PD	27-JUL-1995.		
XX			
PF	23-JAN-1995; 95WO-0080955.		
XX			
PR	21-JAN-1994; 94US-0185359.		
XX			
PA	(SALK) SALK INST BIOLOGICAL STUDIES.		
XX			
PI	Hoekstra MF;		
XX			
DR	WPI: 1995-269419/35.		
XX			
PS	N-PSDB; AAQ929662.		
PT	New monoclonal antibodies against human casein Kinase Class I		
XX	enzymes - useful for purification, and determin. of these enzymes and to		
XX	modulate their receptor -ligand binding, also new hybridomas		
PS	Disclosure; Page 100; 125pp; English.		

	CC	Promoting activity.	
xx	SQ	Sequence 377 AA:	
OY	Query Match	74.3%; Score 1669.5; DB 16;	Length 377;
Dd	Best Local Similarity	84.8%;	Pred. No. 3e-169;
OY	Matches 318; Conservative	21;	Mismatches 27; Indels 9; Gaps 5
OY	21	NSAHCSRPSGSSSGVLMVGPNFNVKKGICGNFGELRGKNLYTNEYVAIKLEPKSR	80
Dd	7	rsgnhtctgty-ssssgvlmvgpnfrvqkkkgcgnfgelrlgknilylneyvaiklepker	65
OY	81	APQLERFRFYQGLSAGHGILPQQVVFFPGCGKYNNMVLLELGRSLDELFDLCDFRTLLKT	140
Dd	66	apqlrleyrfykyqs-gdgilpqvytfgpcgyknamvllellpsledldlcdrftslkt	124
OY	141	VLMIALISLRREYHASKMLIYRDVKPERFLIGROCKNEHYIHIDFCLAKEVIDPEEK	200
Dd	125	vlnialiqistrmeyhsknillyrdvkpenfiligrpnktqvylhlidflakeyldpeek	184
OY	201	KHIYPREHKSLTGTAARYMSINTHLGEOSRRDDEALGHMFYPLRGSIPWGLKADTLK	260
Dd	185	khiyprehksltgtarymsintlhlgkegsrrddleaahgmfmfyllrgslpwglkadtlk	244
OY	261	ERYQGIGTKRNTPREALCENFPBEEMATYYLKRYRLDPFEKKDYELYRTLPTDLFEKKGY	320
Dd	245	eryqigtkrtatrplevlcnfpbeematyylyrvrldffexkdpylkrlftdlfdkrxy	304
OY	321	TEDVAYDMVGPRITPPRVGSVNHDGASAITRESHTHRDRPSGOGPLRMQVYSTNGELN	380
Dd	305	mfdveydwlgdqldrppvavagqdpaiss-nreaqhndkmqgs--knqvassngelnlt	360
OY	381	DDPTG---AHSNAPI 392 : :	
Dd	361	dgpptadvgmhpsqp1 375	
RESULT	7	AAR56530 standard; Protein: 347 AA. AA56530: AC AAR56530; XX DT 17-MAR-1995 (first entry) XX DE Protein kinase (CKIIgamma2Hu). XX KW Protein kinase; immunogen; antibody; protein-tyrosine kinase; KM protein-serine/threonine kinase; recombination; repair; screening; delection; casein kinase. XX OS Homo sapiens. XX XX W09417189-A. XX PD 04-AUG-1994. XX PF 21-JAN-1994; 94MO-USO0795. XX PR 21-JAN-1993; 93US-0008001. PA (SALK) SALK INST BIOLOGICAL STUDIES. XX PI Hoekstra MF; DR WP1, 1994-264102/32. DN N-PDB; AAC70828. XX XX Wild-type and mutant protein kinase genes and encoded PT polypeptide(s) - Useful in screening for compositions which may effect DNA double strand break repair activity XX	

XX WO200171042-A2.
PN 27-SEP-2001.
XX 23-MAR-2001; 2001WO-US09231.
XX 23-MAR-2000; 2000US-191637P.
PR 11-JUL-2000; 2000US-0614150.
XX (PEKE) PE CORP NY.
XX Venter JC, Adams M, Li PMD, Myers EW;
PI WPI; 2001-656860/75.
DR N-PSDB; ABL10653.
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX
XX Disclosure; SEQ ID NO 26442; 21pp + Sequence Listing; English.
XX
XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins
CC (AB57737-AB572072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 422 AA:
SO
Query Match 69.1%; Score 1553; DB 22; Length 422;
Best Local Similarity 70.8%; Pred. No. 9.8e-157;
Matches 294; Conservative 41; Mismatches 52; Indels 28; Gaps 4;
OY 32 SSSSGVLMVGNPNRVGKKGNGNSELRLGKNLYTNEYVAIKLEPIKRAPOLHLEFRY 91
DB 9 sttgytvmgpnfivgkkgngnsefgrlirgknlymnevhakmepmkskdpqihleyrfy 68
OY 92 KOLGSAEGELPOVYFEGPCGKYNAMVELLGPSELEDFDLCDRTFTLTKTYLMAIQLSLR 151
DB 69 kllyshaeqyvevyfypgckkynalmellgspledlfdtcgrfrtlksvlllaigllhr 128
OY 152 MEVYHSKNLYRDVKNPENFLIGROGKKEHVHITDFGLAKKEYIDPETKHHIPYREHKS 211
DB 129 leyvhsrhllyrtdvknpenfligrstkreklhldfqlakeyldldtnhlyprehksl 188
OY 212 TGTARVMSITHTHGKEGSRDDLEALGHMFMYFLRGSIPMOGKADPLKRYOKIGTTR 271
DB 189 tgarvmsitctmngrestrddlealghmfmlyflrsglpadlkerqyqigqctr 248
OY 272 NTFIEALCENFPEEMATYLYRVRLDFFEKPDYEYLTLETFDEFEKKGYFDYADWVGR 331
DB 249 atplevldcghpfeefatyllyrvrrldftecpydflrrlrgdldfdrkygdegefdwtgk 308
OY 332 PIRTPVGSVHVDGASAI---TRESH-----THRRPSGOQPLRN----- 368
DB 309 tmsrtpvgs--lqtshevlispmkdrhntaktakgvaavpdpkpgatlglltpdarh 366
OY 369 ---OVASTNGELNVDDPTGASHNAPITAHAEVVEAEKCCCFKKRKKRKTQR 420
DB 367 gsvqvsvstngelnvddptgashnaptlctgqvevvdetkcccfkfrkkkksrtq 421
RESULT 10
ABB71525

ID ABB71525 standard; Protein: 422 AA.
XX ABB71525;
AC 26-MAR-2002 (first entry)
XX
XX Drosophila melanogaster polypeptide SEQ ID NO 41367.
DE Drosophila melanogaster polypeptide SEQ ID NO 41367.
XX
XX Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical.
XX
XX Drosophila melanogaster.
OS
XX WO200171042-A2.
XX 27-SEP-2001.
XX 23-MAR-2001; 2001WO-US09231.
XX 23-MAR-2000; 2000US-191637P.
PR 11-JUL-2000; 2000US-0614150.
XX (PEKE) PE CORP NY.
XX Venter JC, Adams M, Li PMD, Myers EW;
PI WPI; 2001-656860/75.
DR N-PSDB; ABL15628.
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX
XX Disclosure; SEQ ID NO 41367; 21pp + Sequence Listing; English.
XX
XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins
CC (AB57737-AB572072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 422 AA:
SO
Query Match 69.1%; Score 1553; DB 22; Length 422;
Best Local Similarity 70.8%; Pred. No. 9.8e-157;
Matches 294; Conservative 41; Mismatches 52; Indels 28; Gaps 4;
OY 32 SSSSGVLMVGNPNRVGKKGNGNSELRLGKNLYTNEYVAIKLEPIKRAPOLHLEFRY 91
DB 9 sttgytvmgpnfivgkkgngnsefgrlirgknlymnevhakmepmkskdpqihleyrfy 68
OY 92 KOLGSAEGELPOVYFEGPCGKYNAMVELLGPSELEDFDLCDRTFTLTKTYLMAIQLSLR 151
DB 69 kllyshaeqyvevyfypgckkynalmellgspledlfdtcgrfrtlksvlllaigllhr 128
OY 152 MEVYHSKNLYRDVKNPENFLIGROGKKEHVHITDFGLAKKEYIDPETKHHIPYREHKS 211
DB 129 leyvhsrhllyrtdvknpenfligrstkreklhldfqlakeyldldtnhlyprehksl 188
OY 212 TGTARVMSITHTHGKEGSRDDLEALGHMFMYFLRGSIPMOGKADPLKRYOKIGTTR 271
DB 189 tgarvmsitctmngrestrddlealghmfmlyflrsglpadlkerqyqigqctr 248
OY 272 NTFIEALCENFPEEMATYLYRVRLDFFEKPDYEYLTLETFDEFEKKGYFDYADWVGR 331
DB 249 atplevldcghpfeefatyllyrvrrldftecpydflrrlrgdldfdrkygdegefdwtgk 308

PD 06-SEP-2000.
XX
XX 25-FEB-2000; 2000EP-0301439.
PR 25-FEB-1999; 9905-0121825.
PR 05-MAR-1999; 9905-0123180.
PR 09-MAR-1999; 9905-0123548.
PR 23-MAR-1999; 9905-0125788.
PR 25-MAR-1999; 9905-0126284.
PR 29-MAR-1999; 9905-0126785.
PR 01-APR-1999; 9905-0127462.
PR 06-APR-1999; 9905-0128234.
PR 08-APR-1999; 9905-0128714.
PR 16-APR-1999; 9905-0129845.
PR 19-APR-1999; 9905-0130077.
PR 21-APR-1999; 9905-0130449.
PR 23-APR-1999; 9905-0130510.
PR 28-APR-1999; 9905-0130891.
PR 30-APR-1999; 9905-0132048.
PR 30-APR-1999; 9905-0132407.
PR 04-MAY-1999; 9905-0132484.
PR 05-MAY-1999; 9905-0132485.
PR 06-MAY-1999; 9905-0132486.
PR 07-MAY-1999; 9905-0132487.
PR 11-MAY-1999; 9905-0134256.
PR 14-MAY-1999; 9905-0134218.
PR 14-MAY-1999; 9905-0134219.
PR 14-MAY-1999; 9905-0134221.
PR 14-MAY-1999; 9905-0134370.
PR 18-MAY-1999; 9905-0134768.
PR 19-MAY-1999; 9905-0134941.
PR 20-MAY-1999; 9905-0135124.
PR 21-MAY-1999; 9905-0135353.
PR 24-MAY-1999; 9905-0135629.
PR 25-MAY-1999; 9905-0136021.
PR 27-MAY-1999; 9905-0136392.
PR 28-MAY-1999; 9905-0136782.
PR 01-JUN-1999; 9905-0137222.
PR 03-JUN-1999; 9905-0137528.
PR 04-JUN-1999; 9905-0137502.
PR 07-JUN-1999; 9905-0137724.
PR 08-JUN-1999; 9905-0138094.
PR 10-JUN-1999; 9905-0138547.
PR 14-JUN-1999; 9905-0139119.
PR 16-JUN-1999; 9905-0139453.
PR 17-JUN-1999; 9905-0139492.
PR 18-JUN-1999; 9905-0139454.
PR 18-JUN-1999; 9905-0139455.
PR 18-JUN-1999; 9905-0139456.
PR 18-JUN-1999; 9905-0139457.
PR 18-JUN-1999; 9905-0139458.
PR 18-JUN-1999; 9905-0139459.
PR 18-JUN-1999; 9905-0139460.
PR 18-JUN-1999; 9905-0139461.
PR 18-JUN-1999; 9905-0139462.
PR 18-JUN-1999; 9905-0139463.
PR 18-JUN-1999; 9905-0139750.
PR 18-JUN-1999; 9905-0139763.
PR 21-JUN-1999; 9905-0139817.
PR 22-JUN-1999; 9905-0139899.
PR 23-JUN-1999; 9905-0140353.
PR 23-JUN-1999; 9905-0140354.
PR 24-JUN-1999; 9905-0140695.
PR 28-JUN-1999; 9905-0140823.
PR 29-JUN-1999; 9905-0140991.
PR 30-JUN-1999; 9905-0141287.
PR 01-JUL-1999; 9905-0141642.
PR 01-JUL-1999; 9905-0142154.
PR 02-JUL-1999; 9905-0142055.

PR 06-JUL-1999; 9905-0142390.
PR 08-JUL-1999; 9905-0142803.
PR 09-JUL-1999; 9905-0142920.
PR 12-JUL-1999; 9905-0142977.
PR 13-JUL-1999; 9905-0143542.
PR 14-JUL-1999; 9905-0143624.
PR 15-JUL-1999; 9905-0144005.
PR 16-JUL-1999; 9905-0144085.
PR 16-JUL-1999; 9905-0144086.
PR 19-JUL-1999; 9905-0144325.
PR 19-JUL-1999; 9905-0144331.
PR 19-JUL-1999; 9905-0144332.
PR 19-JUL-1999; 9905-0144333.
PR 19-JUL-1999; 9905-0144334.
PR 19-JUL-1999; 9905-0144335.
PR 20-JUL-1999; 9905-0144352.
PR 20-JUL-1999; 9905-0144632.
PR 20-JUL-1999; 9905-0144684.
PR 21-JUL-1999; 9905-0144814.
PR 21-JUL-1999; 9905-0145086.
PR 21-JUL-1999; 9905-0145088.
PR 22-JUL-1999; 9905-0145085.
PR 22-JUL-1999; 9905-0145087.
PR 22-JUL-1999; 9905-0145089.
PR 22-JUL-1999; 9905-0145192.
PR 23-JUL-1999; 9905-0145145.
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PR 23-JUL-1999; 9905-0145224.
PR 26-JUL-1999; 9905-0145276.
PR 27-JUL-1999; 9905-0145913.
PR 27-JUL-1999; 9905-0145918.
PR 27-JUL-1999; 9905-0145919.
PR 28-JUL-1999; 9905-0145951.
PR 02-AUG-1999; 9905-0146386.
PR 02-AUG-1999; 9905-0146388.
PR 02-AUG-1999; 9905-0146389.
PR 03-AUG-1999; 9905-0146708.
PR 04-AUG-1999; 9905-0147204.
PR 04-AUG-1999; 9905-0147302.
PR 05-AUG-1999; 9905-0147192.
PR 05-AUG-1999; 9905-0147260.
PR 06-AUG-1999; 9905-0147303.
PR 06-AUG-1999; 9905-0147416.
PR 09-AUG-1999; 9905-0147493.
PR 09-AUG-1999; 9905-0147935.
PR 10-AUG-1999; 9905-0148171.
PR 11-AUG-1999; 9905-0148319.
PR 12-AUG-1999; 9905-0148341.
PR 13-AUG-1999; 9905-0148565.
PR 13-AUG-1999; 9905-0148684.
PR 16-AUG-1999; 9905-0149368.
PR 17-AUG-1999; 9905-0149375.
PR 18-AUG-1999; 9905-0149426.
PR 20-AUG-1999; 9905-0149722.
PR 20-AUG-1999; 9905-0149723.
PR 20-AUG-1999; 9905-0149929.
PR 23-AUG-1999; 9905-0149902.
PR 23-AUG-1999; 9905-0149930.
PR 25-AUG-1999; 9905-0150566.
PR 26-AUG-1999; 9905-0150884.
PR 27-AUG-1999; 9905-0151065.
PR 27-AUG-1999; 9905-0151066.
PR 27-AUG-1999; 9905-0151080.
PR 30-AUG-1999; 9905-0151303.
PR 31-AUG-1999; 9905-0151438.
PR 01-SEP-1999; 9905-0151930.
PR 07-SEP-1999; 9905-0152363.
PR 10-SEP-1999; 9905-0153070.
PR 13-SEP-1999; 9905-0153758.
PR 15-SEP-1999; 9905-0154018.
PR 16-SEP-1999; 9905-0154039.
PR 20-SEP-1999; 9905-0154779.
PR 22-SEP-1999; 9905-0155139.

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PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155486.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 41.7%; Score 938; DB 21; Length 476;
Best Local Similarity 54.2%; Pred. No. 5.8e-91;
Matches 180; Conservative 60; Mismatches 84; Indels 8; Gaps 5;
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QY 38 LMVGNFVGVKKGNGNNGELRLGNLYTNEVAIKLEPIKSRAPQDLHLEFRFYQLOLSA 97
DB 3 lviqgkfkigkigsgsfgylylgvavgtgeevavklevkthpqlhyesklyml-qg 61
QY 98 GEGLPQVYVFGPCGKYNNMVELLGPSELDLDCDRFTTKTYMIAIQLSRMEYVHS 157
DB 62 gsglpnlkwfgyegdyvawidllypsledlfnycnrkltkvtvmladqllnvefmlt 121
QY 158 KNLIRDVKPNENFLIGROGNKKEHYIHIDFLAKKEYIDPETKRHIPYREKSLTGARY 217
DB 122 rgfihrdtkpndflmg1--gktangvylidfgygkkyrdlqthkhlpyrenknlgtary 179
QY 218 MSINTHLCKEGRDDELALGHMFWYFLRGLSPWOGKADLTKEERYOKIGTKRNTPIEA 277
DB 180 asvnhlvgvsgirdldslgyvlnmyflkgsipwglkagtkkgydrdisekvstplev 239
QY 278 LCENPEEMATYLYRVRLDPEFEKPDYELRTLFDTLFEKKGYTDYVDMWGRIRIPV 337
DB 240 lcknpsfeyfhyrcslrfdckpdylylkrllfdlfliregyqdyfdwcvlkyr-q1 298
QY 338 GSVHVDGASATRESHTHRDRPSGOQPLRNO 369
DB 299 gs---ssgsssrtrh-httakpgfnadplercq 326

RESULT 13
AAR56531
ID AAR56531 standard; Protein: 415 AA.
XX
AC AAR56531;
```

```
XX 17-MAR-1995 (first entry)
DT
XX Protein kinase (CKIdeltaHu).
DE
XX Protein kinase; immunogen; antibody; protein-tyrosine kinase;
KW protein-serine/threonine kinase; recombination; repair; screening;
KW detection; casein kinase.
OS Homo sapiens.
XX
XX WO9417189-A.
XX
XX 04-AUG-1994.
XX
XX 21-JAN-1994; 94MO-US00795.
XX
XX 21-JAN-1993; 93US-0008001.
XX
XX (SALK ) SALK INST BIOLOGICAL STUDIES.
XX
XX Hoekstra ME;
XX
XX WPL 1994-264102/32.
XX
XX N-PSDB: AAO70829.
XX
XX Wild-type and mutant protein kinase genes and encoded
XX polypeptide(s) - useful in screening for compositions which may
XX effect DNA double strand break repair activity
XX
XX Claim 11; Page 107-108; 121pp; English.
```

This sequence is a protein kinase similar to the HRR25 protein of *Saccharomyces cerevisiae* which is described in AAR56519. Host cells stably transformed with the protein kinase encoding DNA may be used for the expression of the protein kinase such that the expressed protein is "displayed" on the host cell surface. The cells may then be used as immunogen for the production of antibodies. The host cells may also be used for the large scale production of the protein kinase, the expressed protein being either isolated from the cell surface or from the culture medium. Recombinant HRR25 like proteins display a number of properties which are unique among the eukaryotic protein kinases e.g. the HRR25 protein possesses both protein-tyrosine kinase and protein-serine/threonine kinase activities. Also, HRR25 operates to promote repair of DNA strand breaks at a specific nucleotide sequence and is the only protein kinase known to have such recombination/repair promoting activity. Recombinant HRR25-like proteins and host cells expressing them are useful in screening methods designed to examine the effects of various compositions on DNA break repair and protein kinase activities of the protein. The HRR25-like proteins are casein kinase_class I protein kinases.

Sequence 415 AA;

```
Query Match 41.6%; Score 936; DB 15; Length 415;
Best Local Similarity 47.2%; Pred. No. 7.7e-91;
Matches 188; Conservative 75; Mismatches 97; Indels 38; Gaps 6;

QY 38 LMVGNFVGVKKGNGNNGELRLGNLYTNEVAIKLEPIKSRAPQDLHLEFRFYQLOLSA 97
DB 3 lviqgnyrlgrkligsgsfgyldltdlaageavaklecvtkhqpqlhyeskykm-qg 61
QY 98 GEGLPQVYVFGPCGKYNNMVELLGPSELDLDCDRFTTKTYMIAIQLSRMEYVHS 157
DB 62 gvglpnlrwcgaegdynmwemllypsledlfnfcsrfskltvllladqmsrleyhs 121
QY 158 KNLIRDVKPNENFLIGROGNKKEHYIHIDFLAKKEYIDPETKRHIPYREKSLTGARY 217
DB 122 knfihrdvknfndflmg1--gkkgnlvylidfgyakkydarthqhlpyrenknlgtary 179
QY 218 MSINTHLCKEGRDDELALGHMFWYFLRGLSPWOGKADLTKEERYOKIGTKRNTPIEA 277
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Db      180 aslnthlgtesrrddleslgyvlnmylnhlslpwqgkkaatkrgkyerisekkmsphiev 239
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY      278 LCENEPEEMATYLRVYVERLDFEKKPDEYLRITLFTDLEKKGYTFDYADWGRPIPTPV 337
      ||: ||: ||||| ||: ||: ||||| ||||| ||||| ||||| ||||| |||||
Db      240 lckypseafatylncfslrfdckpdyisrlqrlfnlfnhgdfsydyfaw----- 250
QY      338 GSVHVDGSASATRESHTRDRPESQOQLRNQVVSSTNG-----ELNWDPT 384
      : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db      291 --nmllkfygasaadda--eerirdeerellhsrmpatrglpstasgrlrgtqgevappptpl 346
QY      385 GAHSNAPITAAHEVEVEAKKCCFFFRKKRKTQAKRH 422
      : ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
Db      347 tpehtantsprvysgme-----tekvsmrlnlr 375

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RESULT 14
AAR76627
ID AAR76627 standard; Protein; 415 AA

AC	AAR76627;
XX	
DT	25-JAN-1996 (first entry)

Human HRR25-like casein-kinase-I CKI- δ -Hu protein.

KW Caseln-kinase-I; HRR25; protein-tyrosine-kinase; CKI-delta-HU;
KW protein-serine/chreonline-kinase; enzyme; DNA repair;
KW DNA recombination.

Homo sapiens.

PN W09519993-A1.

PD 27-JUL-1995.

PF 23-JAN-1995; 95WO-US00955.

PR 21-JAN-1994; 94US-0185359.

PA (SALK) SALK INST BIOLOGICAL. STUDIES.

PI Hoekstra MF;

DR WPT; 1995-269419/35.

XX

PT enzymes - useful for purificn. and determ. of these enzymes

PS Disclosure; Page 107; 125pp; English.

CC This human casin-kinase-I (CRI-delta-hu) protein which is a homolog
CC of a DNA recombination and repair protein HR23.5 (HO and/or
CC radiation repair) possesses both protein-tyrosine-kinase and protein
CC serine/threonine-kinase activities. HR23.5 operates to promote repair
CC of DNA strand breaks at a specific nucleotide sequence and is the
CC only protein-kinase known to have such recombination/repair
CC promoting activity.

SQ **Sequence** **415 AA;**

Query Match	41.6%	Score 936	DB 16	Length 415
Best Local Similarly	47.2%	Pred. No. 7.7e-91		
Matches 188; Conservative	75	Mismatches 97	Indels 38	Gaps 6

Oy 38 LAMGPNFVKKKICCGNGBELRLCKNTLYMEYVAIKLEPIRSRDPOLHLEPRFKQUGSA 97
|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::
Dd 3 lrvnmyrlgklysgsfddilylgtlaageevakilecvttknpqjhieeklykhmm-qg 61

Oy 98 GEGHPQYYVFSPCKRYANMVLLEGPSLEDLFDLCDBTFTLKTYLMALIQLLSMNEYVHS 157

[illegible]

RESULT 15
AAG45810
ID AAG45810 standard; Protein; 468 AA

AC AAG45810

DT 18-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 57559

KM Protein identification; signal transduction pathway; metabolic pathway;
KM hybridisation assay; genetic mapping; gene expression control; promoter
KM termination sequence.

OS Arabidopsis thaliana.

PN EP1033405-A2

PD 06-SEP-2000.

PF 25-FEB-2000; 2000EP-0301439

PR 25-FEB-1999; 99US-0121825

PR 09-MAR-1999; 99US-0123548

PR 25-MAR-1999; 99US-0126264

PR 01-APR-1999; 99US-0127462

PR 08-APR-1999; 99US-0128714

PR	19-APR-1999;	99US-0130077
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PR 23-APR-1999; 99US-0130510

PR 28-APR-1999; 99US-0131449

PR 30-APR-1999; 99US-0132407

PR 05-MAY-1999; 99US-0132485

PR 06-MAY-1999; 99US-0132487

PR 11-MAY-1999; 99US-0134256

PR 14-MAY-1999; 99US-0134219

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PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
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PR 21-OCT-1999; 99US-0160741.
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PR 21-OCT-1999; 99US-0160770.
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PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.

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OH protein - protein search, using sw model

Run on: August 17, 2002, 19:23:15 ; Search time 24.87 seconds

(without alignments)
414.459 Million cell updates/sec

Title: US-09-765-068-2

Perfect score: 2248
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 2442594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep: *
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6: /cgn2_6/ptodata/1/1aa/Backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	1669.5	74.3	377	1	US-08-454-097-31 Sequence 31, Appl
2	1669.5	74.3	377	3	US-08-185-359-31 Sequence 31, Appl
3	1571.5	69.9	347	1	US-08-454-097-33 Sequence 33, Appl
4	1571.5	69.9	347	3	US-08-185-359-33 Sequence 33, Appl
5	946.5	42.1	416	3	US-09-100-664A-9 Sequence 9, Appl
6	936	41.6	415	1	US-08-454-097-35 Sequence 35, Appl
7	936	41.6	415	3	US-08-185-359-35 Sequence 35, Appl
8	924	41.1	365	1	US-08-447-500-4 Sequence 4, Appl
9	924	41.1	365	3	US-08-454-097-4 Sequence 4, Appl
10	924	41.1	365	1	US-08-454-097-4 Sequence 4, Appl
11	924	41.1	365	3	US-09-100-664A-13 Sequence 13, Appl
12	924	41.1	365	3	US-08-185-359-4 Sequence 4, Appl
13	923.5	41.1	319	3	US-09-100-664A-10 Sequence 10, Appl
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15	907.5	40.4	400	1	US-08-454-097-6 Sequence 6, Appl
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20	876	39.0	440	3	US-09-100-664A-3 Sequence 3, Appl
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22	862.5	38.4	325	1	US-08-454-097-8 Sequence 8, Appl
23	862.5	38.4	325	1	US-08-453-866-8 Sequence 8, Appl
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25	862.5	38.4	337	1	US-08-447-500-10 Sequence 10, Appl
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27	862.5	38.4	337	1	US-08-453-866-10 Sequence 10, Appl

28	862.5	38.4	337	3	US-09-100-664A-11 Sequence 11, Appl
29	862.5	38.4	337	3	US-09-100-664A-12 Sequence 12, Appl
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37	847.5	37.7	364	1	US-08-454-097-10 Sequence 10, Appl
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44	326.5	14.5	396	2	US-08-878-989-16 Sequence 16, Appl
45	326.5	14.5	396	4	US-09-272-796-16 Sequence 16, Appl

ALIGNMENTS

RESULT 1
US-08-454-097-31
Sequence 31, Application US/08454097
Patent No. 5686412
GENERAL INFORMATION:
APPLICANT: Hoechst, Merl F.
TITLE OF INVENTION: Protein Kinases
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESSES:
ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sears Tower
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,097
FILING DATE: 30-MAY-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/185,359
FILING DATE: 21-JAN-1994
APPLICATION NUMBER: US 08/008,001
FILING DATE: 21-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/728,783
FILING DATE: 03-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: No. 5686412and, Greta E.
REGISTRATION NUMBER: 35,302
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 377 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-454-097-31
Query Match 74.3%, Score 1669.5, DB 1, Length 377;

Best Local Similarity 84.8%, Pred. No. 2.8e-161;
Matches 318; Conservative 21; Mismatches 27; Indels 9; Gaps 5;
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QY 381 DDPFG--AHSNAPI 392
Db 361 DDPFG--AHSNAPI 375
RESULT 2
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; Sequence 31, Application US/08185359
; Patent No. 6060296
; GENERAL INFORMATION:
; APPLICANT: Hoechst, Merl F.
; TITLE OF INVENTION: Protein Kinases
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive, 6300 Sears Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PC-DOS/MS-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/185,359
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/008,001
; FILING DATE: 21-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/728,783
; FILING DATE: 03-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6060296and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/31853
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 377 amino acids

TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-185-359-31
Query Match 74.3%, Score 1669.5; DB 3; Length 377;
Best Local Similarity 84.8%, Pred. No. 2.8e-161;
Matches 318; Conservative 21; Mismatches 27; Indels 9; Gaps 5;
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QY 321 TFDYAVDWVGRPIPTPVGSVHVDGSAITRSHTHRDRPSQOQLRNQVYSTNGELNV 380
Db 305 MEDYEDWIGKQLPTPVAVQODPALSS-NREAHORHDKMOOS--KNQVYSTNGELNV 360
QY 381 DDPFG--AHSNAPI 392
Db 361 DDPFG--AHSNAPI 375
RESULT 3
US-08-454-097-33
; Sequence 33, Application US/08454097
; Patent No. 5686412
; GENERAL INFORMATION:
; APPLICANT: Hoechst, Merl F.
; TITLE OF INVENTION: Protein Kinases
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive, 6300 Sears Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PC-DOS/MS-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/454,097
; FILING DATE: 30-MAY-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/185,359
; FILING DATE: 21-JAN-1994
; APPLICATION NUMBER: US 08/008,001
; FILING DATE: 21-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/728,783
; FILING DATE: 03-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5686412and, Greta E.

REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/31853
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 347 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-454-097-33

Query Match 69.9%; Score 1571.5; DB 1; Length 347;
Best Local Similarity 84.9%; Pred. No. 2,2e-151;
Matches 298; Conservative 19; Mismatches 25; Indels 9; Gaps 5;

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RESULT 4
US-08-185-359-33
Sequence 33, Application US/08185359
Patent No. 6060296
GENERAL INFORMATION:
APPLICANT: Hoechst, Merl F.
TITLE OF INVENTION: Protein kinases
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sears Tower
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/185,359
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/008,001
FILING DATE: 21-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/728,783

FILING DATE: 03-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: No. 6060296and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/31853
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 347 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-185-359-33

Query Match 69.9%; Score 1571.5; DB 3; Length 347;
Best Local Similarity 84.9%; Pred. No. 2,2e-151;
Matches 298; Conservative 19; Mismatches 25; Indels 9; Gaps 5;

QY 45 RVGKIGCGNGFELRLGKNTLYNEVAIKLEPIKSRAPQLHLEYRKYQLSGAGELPOV 104
DB 1 RVGKIGCGNGFELRLGKNTLYNEVAIKLEPIKSRAPQLHLEYRKYQLSGAGELPOV 59
QY 105 YFGPGCKYNNMVELLSPLEDFDLCDRTFTLKTVMIAIQLSRMEYHSHKLLIYRD 164
DB 60 YFGPGCKYNNMVELLSPLEDFDLCDRTFTLKTVMIAIQLSRMEYHSHKLLIYRD 119
QY 165 VKPENFLIGROGNKKEHYIHIDFGLAKLEYIDPETKKHIPPYREHNSLGTARYSINTHL 224
DB 120 VKPENFLIGROGNKKEHYIHIDFGLAKLEYIDPETKKHIPPYREHNSLGTARYSINTHL 179
QY 225 GKEOSRRDDALGHEMYFLRGSIPMOGLKADTLKERYOKIGDKRATPIEALCENPE 284
DB 180 GKEOSRRDDALGHEMYFLRGSIPMOGLKADTLKERYOKIGDKRATPIEALCENPE 238
QY 285 EMATYLRVRRLLDFEKKDYELRTLTDLFEKKGYTEVDYADWGRDIPYGVSHVDS 344
DB 239 EMATYLRVRRLLDFEKKDYELRTLTDLFEKKGYTEVDYADWGRDIPYGVSHVDS 298
QY 345 GASAITRESHTHRDPSQQOPLRNQVVSSTNGELNVDDPTG---AHSNAPI 392
DB 239 ALSS-NREAHQRDKMOOS---KNQVVSSTNGELNVDDPTADYQMHPSQPL 345

RESULT 5
US-09-100-664A-9
Sequence 9, Application US/09100664A
Patent No. 6057129
GENERAL INFORMATION:
APPLICANT: YOUNG, MICHAEL W.
APPLICANT: KLOSS, BRIAN
APPLICANT: BLAU, JUSTIN
APPLICANT: PRICE, JEFFREY
TITLE OF INVENTION: A NOVEL CLOCK GENE AND METHODS OF USE
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/100,664A

FILING DATE: 19-JUN-1998
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Jackson Esq., David A.
 REGISTRATION NUMBER: 26,742
 REFERENCE/DOCKET NUMBER: 600-1-221
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201-487-5800
 TELEFAX: 201-343-1684
 TELETYPE: 133521
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 416 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHEICAL: NO
 US-09-100-664A-9

Query Match 42.1%, Score 946.5; DB 3; Length 416;
 Best Local Similarity 51.4%, Pred. No. 9,1e-88;
 Matches 181; Conservative 67; Mismatches 89; Indels 15; Gaps 3;

QY 38 LMVGNFVVKRIGCGNGELRLGKNTNEVAIKLEPIKRAPOLHLEVFYKOLSA 97
 DB 3 LRVGNRYLRKRGISGSGDIYLGANIASGEVAIKLECVTKHQHIESFTYMM-OG 61
 QY 98 GEGLEOVYVYFGPCGKYNMAMVLELLGSPLEDFDLCDRTFTTKTYLMAIQLSRMEYHS 157
 DB 62 GVGISITMCGAEGDYNNVMWELLGSPLEDFLNFCSRKFSUKTYLLADQMSRIEYHS 121
 QY 158 KNLIRVYKPFENFLIGROGNKEHYIHIIDGLAKLEYIDPEKKHIPPYREKSLGTARY 217
 DB 122 KNFIRDVKPNFNLMLG--GKGNLYIIDGLAKRYRDARTHOIIPYREKNTLTGTARY 179
 QY 218 MSINTHLKEOSRRDDELALGHMFYFLRGLPMOGLKADTLKERYOKIGDKRNTPIEA 277
 DB 180 ASINTHLKEOSRRDDELALGHMFYFLRGLPMOGLKADTLKERYOKIGDKRNTPIEA 239
 QY 278 LCENPEEMATYLRVYRRLDPEKPDYELRTLTDLFEKKGYTDYAYDVGRIPIPPV 337
 DB 240 LCKGVPSEFAYLNCRSRLRFDKPDYSLRQLFRNLFRHOGFSYDYVDM----- 290
 QY 338 GSVHVDGASAITRESHTHRDRPSOQOPLRNQVSSSTNGELNVDDPTGAHSN 389
 DB 291 --NMKFGAARNPEDVDREHERHEREMGOLRGSAATRALPPGPPTGATAN 339

RESULT 6
 US-08-454-097-35
 Sequence 35, Application US/08454097
 Patent No. 5686412
 GENERAL INFORMATION:
 APPLICANT: Hoechst, Merl F.
 TITLE OF INVENTION: Protein kinases
 NUMBER OF SEQUENCES: 57
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 STREET: 233 South Wacker Drive, 6300 Sears Tower
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60606-6402
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/454,097
 FILING DATE: 30-MAY-1995

CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/185,359
 FILING DATE: 21-JAN-1994
 APPLICATION NUMBER: US 08/008,001
 FILING DATE: 21-JAN-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/728,783
 FILING DATE: 03-JUL-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: No. 5686412and, Greta E.
 REGISTRATION NUMBER: 35,302
 REFERENCE/DOCKET NUMBER: 27866/31853
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312-474-6300
 TELEFAX: 312-474-0448
 TELETYPE: 25-3856
 INFORMATION FOR SEQ ID NO: 35:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 415 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-454-097-35

Query Match 41.6%, Score 936; DB 1; Length 415;
 Best Local Similarity 47.2%, Pred. No. 1,1e-86;
 Matches 188; Conservative 75; Mismatches 97; Indels 38; Gaps 6;

QY 38 LMVGNFVVKRIGCGNGELRLGKNTNEVAIKLEPIKRAPOLHLEVFYKOLSA 97
 DB 3 LRVGNRYLRKRGISGSGDIYLGDIAGGEVAIKLECVTKHQHIESFTYMM-OG 61
 QY 98 GEGLEOVYVYFGPCGKYNMAMVLELLGSPLEDFDLCDRTFTTKTYLMAIQLSRMEYHS 157
 DB 62 GVGISITMCGAEGDYNNVMWELLGSPLEDFLNFCSRKFSUKTYLLADQMSRIEYHS 121
 QY 158 KNLIRVYKPFENFLIGROGNKEHYIHIIDGLAKLEYIDPEKKHIPPYREKSLGTARY 217
 DB 122 KNFIRDVKPNFNLMLG--GKGNLYIIDGLAKRYRDARTHOIIPYREKNTLTGTARY 179
 QY 218 MSINTHLKEOSRRDDELALGHMFYFLRGLPMOGLKADTLKERYOKIGDKRNTPIEA 277
 DB 180 ASINTHLKEOSRRDDELALGHMFYFLRGLPMOGLKADTLKERYOKIGDKRNTPIEA 239
 QY 278 LCENPEEMATYLRVYRRLDPEKPDYELRTLTDLFEKKGYTDYAYDVGRIPIPPV 337
 DB 240 LCKGVPSEFAYLNCRSRLRFDKPDYSLRQLFRNLFRHOGFSYDYVDM----- 290
 QY 338 GSVHVDGASAITRESHTHRDRPSOQOPLRNQVSSSTNGELNVDDPTGAHSN 384
 DB 291 --NMKFGASRAADDA--ERERDRERLRSRNATIGLSTASGRLRGQEVAFPIPL 346
 QY 385 GAHSNAPITTAHAEEVEEACCCCFKRRKRTAQRK 422
 DB 347 TPTSHANTSPRPVSGME-----RERYSMRLHR 375

RESULT 7
 US-08-185-359-35
 Sequence 35, Application US/08185359
 Patent No. 6060296
 GENERAL INFORMATION:
 APPLICANT: Hoechst, Merl F.
 TITLE OF INVENTION: Protein kinases
 NUMBER OF SEQUENCES: 57
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 STREET: 233 South Wacker Drive, 6300 Sears Tower
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA

ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/185,359
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/008,001
FILING DATE: 21-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/728,783
FILING DATE: 03-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: No. 6060296and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/31853
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 415 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-185-359-35

Query Match 41.6%; Score 936; DB 3; Length 415;
Best Local Similarity 47.2%; Pred. No. 1.1e-86;
Matches 188; Conservative 75; Mismatches 97; Indels 38; Gaps 6;
DB 3 LRVGRNRYLGGKRIKSGSGFDIYLTGDIAGAEVAIKLECVTKRHPOLHIEKRIKMM-OG 61
98 GEGLPVYYRPGCGKYNMAMVELLGPSPLEDFDLCDDRTFTLTVMIAIQLSRMEYVHS 157
158 KNLIRDYKPNFLRGKGNKKEVHIIDFGLAKEYIDPETKKHPIPREKHSITGRTY 217
122 KNFIHRDVKPNFLMGL--GRKGNLVIYIDFGLAKEYIDARTHOHPIPREKKNLTGTARY 179
218 MSINTHLGKESRRDDLEALGHMFMFLRGLSPWOGKADTLKERYOKIGDTKRNPPIEA 277
180 ASINTHLGIESRRDDLESLVLTFTNLSLPWOGKAAATKRKRYETISKKMSTPIEV 239
278 LCENPEEMATYLRVYRLDFEFKPDYEXYLTFTLFEKKGYFDVAYVDMVGRPIPTV 337
240 LCKGIPSEFATYLNFCSLRDRKPDYSYLRQLFRNLFHRGFSYDYEDM----- 290
338 GSVHVDGASATITRESHTHRPDSOQPLRNQVYSTNG-----ELNVDDPT 384
291 --NNMKFGASRAADDA--ERERRDRERLRHSRNPATGTGLSTASGRLRGTQEVAPPTPL 346
385 GAHSNAPITTAHEVYVEAKCCCFKRRKKTQNRKH 422
347 TPTSHTANTSPRVSGME-----RERKVSMLHR 375

RESULT 8
US-08-447-500-4
Sequence 4, Application US/08447500
Patent No. 5627064
GENERAL INFORMATION:
APPLICANT: Hoechst, Merl F.
TITLE OF INVENTION: PROTEIN KINASES

NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East, Suite 500
CITY: Los Angeles
STATE: CA
COUNTRY: USA
ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/447,500
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/008,001
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Wetherell, Ph.D., John R.
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: PD-2458
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 365 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-447-500-4

Query Match 41.1%; Score 924; DB 1; Length 365;
Best Local Similarity 49.2%; Pred. No. 1.4e-85;
Matches 190; Conservative 63; Mismatches 75; Indels 58; Gaps 9;
DB 5 LRIGNKRYIGRKIGSGSGFDIYLTGTVNVSGBEVAIKLESTRKHPOLLEYEVYRIL-SG 63
98 GEGLPVYYRPGCGKYNMAMVELLGPSPLEDFDLCDDRTFTLTVMIAIQLSRMEYVHS 157
64 GVGIPFVWFGVECDYNNAMVDLGPSPLEDFNFCNKRFSLTQVLLADQLSRIEFTHS 123
158 KNLIRDYKPNFL--IGROGNKKEVHIIDFGLAKEYIDPETKKHPIPREKHSITGRTA 215
124 KSFILRDKPNFLMGLGKRGNO---VNIIIDFGLAKEYIDARTHOHPIPREKKNLTGTA 179
216 RYMSINTHLGKESRRDDLEALGHMFMFLRGLSPWOGKADTLKERYOKIGDTKRNPPI 275
180 RYASINTHLGIESRRDDLESLVLTFTNLSLPWOGKAAATKRKRYETISKKMSTPIEV 239
276 EALCENPEEMATYLRVYRLDFEFKPDYEXYLTFTLFEKKGYFDVAYVDMVGRPIPT 335
240 EYLGRFPQESITLNTYRSIRFDKPDYATLRKLFRLFCQSTEFDYEDM----- 292
336 PVGSHVDGASATITRESHTHRPDSOQ-----PLRN---QVYSS 373
293 -----TLKKTQDDOHOQOOLQSLATPOALNPPREBSFNNYQKQNPDE 338
374 TNGELN-----VDDP--TGA-HSNAP 391
339 KGGDINTTVPYIINDPSATGAQYINRP 364

RESULT 9
US-08-454-097-4
Sequence 4, Application US/08454097
Patent No. 5686412

```

GENERAL INFORMATION:
APPLICANT: Hoechst, Merl F.
TITLE OF INVENTION: Protein kinases
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sears Tower
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,097
FILING DATE: 30-MAY-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/185,359
FILING DATE: 21-JAN-1994
APPLICATION NUMBER: US 08/008,001
FILING DATE: 21-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/728,783
FILING DATE: 03-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: No. 5686412and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/31853
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 365 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-454-097-4

Query Match 41.1%, Score 924; DB 1; Length 365;
Best Local Similarity 49.2%, Pred. No. 1.4e-85;
Matches 190; Conservative 63; Mismatches 75; Indels 58; Gaps 9;

```

```

OY 374 TNGELN-----VDDP--TGA-HSNAP 391
DB 339 KCGDINTVPIYNDPSATGAQYINRP 364

RESULT 10
US-08-453-866-4
Sequence 4, Application US/08453866
Patent No. 5756289
GENERAL INFORMATION:
APPLICANT: Hoechst, Merl F.
TITLE OF INVENTION: PROTEIN KINASES
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East, Suite 500
CITY: Los Angeles
STATE: CA
COUNTRY: USA
ZIP: 90067

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/453,866
FILING DATE: 30-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/008,001
FILING DATE: 20-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Wetherell Ph.D., John R.
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: PD-2458
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5100
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 365 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-453-866-4

Query Match 41.1%, Score 924; DB 1; Length 365;
Best Local Similarity 49.2%, Pred. No. 1.4e-85;
Matches 190; Conservative 63; Mismatches 75; Indels 58; Gaps 9;

```

Db 339 KGDINTTPVINDPSATGAQYINRP 364

RESULT 10

T43314
Casein kinase-1 homolog, isoform ck13 - fission yeast (Schizosaccharomyces pombe)

C/Species: Schizosaccharomyces pombe
C/Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 21-Jul-2000

C/Accession: T43314; T37890
R:Kitamura, K.; Yamashita, I.
Gene 214, 131-137, 1998

A/Title: Identification of a novel casein kinase-1 homolog in fission yeast Schizosaccharomyces pombe
A/Reference number: Z22417; MID:98322261

A/Accession: T43314
A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-439 <RT>

A/Cross-references: EMBL:AB010643; NID:93452569; PIDN:BA32482.1; PID:93452570

R:Reger, M.; McDonough, R.C.; Rajandream, M.A.; Barrell, B.G.
Submitted to the EMBL Data Library, September 1999

A/Reference number: Z21752

A/Accession: T37890

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-439 <RT>

A/Cross-references: EMBL:AL117390; PIDN:CA55846.1; GSPDB:GND0066; SPDB:SPAC1805.05

A/Experimental source: strain 972h; cosmid c1805

C/Genetics:

A/Gene: ck13; SPAC1805.05

A/Map position: 1

A/Intons: 45/3; 69/1; 118/3

Query Match 41.1%; Score 924; DB 2; Length 439;
Best Local Similarity 46.1%; Pred. No. 3e-48;

Matches 196; Conservative 63; Mismatches 126; Indels 40; Gaps 6;

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QY 31 SSSSSGVLAMPNFRVCKKIGCGFGLRLGKNTYNEYVAIKLEPKSRAPOLHLEFRF 90
    ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
DB 2 STSSHNVVGVHVRKKGIGESFGMLFGVNLINNOPIALKESSKSEVPOLRDEYLT 61
QY 91 YKOGSAGEGLPQVYFPGCKYNAVLELGPSELEDFDLCDRTFTKTYLMTAIOLES 150
    ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
DB 62 YKLIMGL-PGIPSVYYGEGSMYLVMDLIGSELEDFDYCGRRSPKTYAMAKOMIT 120
QY 151 RMEYVHSHKNTLYRDVKNFLIGROGKKEHVHIIIDFLAKEYIDETKHHIPREHS 210
    ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
DB 121 RIQSVHRHFYRDKPNDLIGPPGKTEVYAVDFGAKQYRDKTHVHRPNEHS 180
QY 211 LTGTARMSINTHLGKQSRDDLEALGHPMTFLKGSLEPMOGLKADTLKERYKIDTK 270
    ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
DB 181 LSGTARMSINTHLGROSRDDLESGHVMYFLRGSLEPMOGLKATNKOKYEIEKK 240
QY 271 RNPFEALCENPEEMATYLRVYRLDFEFKPDVEYLTFTDLEFKKGTFDVAYVMV- 329
    ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
DB 241 QVTPLECEYEPREYLYMAYRNLGYEAPDYDLSLPSDLLRINETDQKIDMTL 300
QY 330 ---GRPIPTFGSVHV-----DSGASAITRESHTRD--RPSOQPLRNQVSS 373
    ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
DB 301 LNNKGQMSAKQHVQRRHGTGNNRQSTIPYARTQNNLSSPSKTPVANNVDAS 360
QY 374 T-----NGLNVDPTGSHNAPITAH-AEVEVVEAKCCCFEK 411
    ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
DB 361 VATQKDIPIGRKASPQVQOQOQSSAQOQOPQVREOPAPOTPTOPTOQAAAPAPSK 420
QY 412 KRRKK 416
    ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
DB 421 KSRKK 425
    ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

```

RESULT 11

A55661

protein kinase ADK1 - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cross)
C/Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 10-Dec-1999

C/Accession: A55661

R:Ali, N.; Halfter, U.; Chua, N.H.
J. Biol. Chem. 269, 31626-31629, 1994

A/Title: Cloning and biochemical characterization of a plant protein kinase that phosphotransfers

A/Reference number: A55661; MID:95081107

A/Accession: A55661

A/Status: preliminary; nucleic acid sequence not shown; not compared with conceptual

A/Molecule type: mRNA

A/Residues: 1-319 <Ali>

A/Cross-references: GB:U48779; NID:91216483; PIDN:ABA7968.1; PID:91216484

C/Superfamily: kinase-related transforming protein; protein kinase homology

F:7-279/Domain: protein kinase homology <Kin>

Query Match 41.1%; Score 923.5; DB 2; Length 319;

Best Local Similarity 55.4%; Pred. No. 2.2e-48;

Matches 174; Conservative 61; Mismatches 72; Indels 7; Gaps 4;

```

QY 38 LMGPNFRVGGKIGCGFGLRLGKNTYNEYVAIKLEPKSRAPOLHLEFRFKOGSA 97
    ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
DB 3 LVIGGKFKLKRKIGSGFGLYLGINVOTGEVAVKLESVYTKRHPOLHYESKLYML-OG 61
QY 98 GEGLPQVYFPGCKYNAVLELGPSELEDFDLCDRTFTKTYLMTAIOLESMEYVHS 157
    ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
DB 62 GTGPNKRWYGEVDVYVYIDLGPSELEDFENCKRLSKTYLMDOLINVEFMHT 121
QY 158 KNTLYRDVKNFLIGROGKKEHVHIIIDFLAKEYIDETKHHIPREHS LGTARY 217
    ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
DB 122 RGLFHRDKPNDLIMGL--GKANQVYIIDGLGKTKRDTGTHHIDYREKNTLGATARY 179
QY 218 MSINTHLGKQSRDDLEALGHPMTFLKGSLEPMOGLKADTLKERYKIDTKRNTPEA 277
    ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
DB 180 ASVNTHLGVEQSRDDLEALGYVLYKLSLPMOGLKAGTKOKYRISSEKVAIPLEV 239
QY 278 LCNFPEEMATYLRVYRLDFEFKPDVEYLTFTDLEFKKGTFDVAYVMVGRPIPPV 337
    ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
DB 240 LCKNQSEVYSTRYCSLRFDDKPDYSLKRLRDLFIRGTFDYVDMTVLKYR-OT 298
QY 338 GSVHVDGASAITR 351
    ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
DB 299 GS---SSGSSSRTR 309
    ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

```

RESULT 12

T04626

probable protein kinase (EC 2.7.1.-) F2009.240 - Arabidopsis thaliana

C/Species: Arabidopsis thaliana (mouse-ear cross)

C/Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 10-Dec-1999

C/Accession: T04626

R:Bevan, M.; Rose, M.; Hempel, S.; Ertlan, K.D.; Hohenseil, J.; Mewes, H.W.; Mayer, K.

Submitted to the Protein Sequence Database, October 1998

A/Reference number: 215380

A/Accession: T04626

A/Molecule type: DNA

A/Residues: 1-321 <BEV>

A/Cross-references: EMBL:AL021749

C/Genetics:

A/Map position: 4

A/Intons: 26/1; 39/3; 63/1; 112/3; 144/3; 168/2; 189/1; 210/2; 238/3; 281/1

A/Note: F2009.240

C/Superfamily: kinase-related transforming protein; protein kinase homology

C/Keywords: phosphotransferase

F:7-279/Domain: protein kinase homology <Kin>

Query Match 41.0%; Score 921; DB 2; Length 321;

Best Local Similarity 54.4%; Pred. No. 3.2e-48;

Matches 173; Conservative 57; Mismatches 74; Indels 14; Gaps 3;

RESULT 15

C71405

Probable casein kinase I - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

A:Variety: Columbia

C:Date: 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 22-Oct-2001

C:Accession: C71405

R:Bevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; Dijk

P.; Medler, H.; Wedler, E.; Wambutt, R.; Weitzengraber, T.; Pohl, T.M.; Terry, N.; Giel

Nature 391, 485-488, 1998

A:Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Puigdomenech

erhoff, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.; Ans

C.; Chalvatzis, N.

A:Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis thal

A:Reference number: A71400; MIMD:9812113

A:Accession: C71405

A:Status: Preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-457 <BEV>

A:Cross-references: GB:297336; NID:g2244788; PID:e326884; PID:g2244791

C:Genetics:

A:Map position: 4COP9-4G3845

C:Superfamily: kinase-related transforming protein; protein kinase homology

F:13-285/Domain: protein kinase homology <KIN>

Query Match 40.8%; Score 918; DB 2; Length 457;

Best Local Similarity 44.6%; Pred. No. 7.2e-48;

Matches 189; Conservative 76; Mismatches 95; Indels 64; Gaps 10;

QY 39 MGNPNFRVKKIGGNGELRLGNLTNEYVAKLEPIKSRAPQLHEVRYKQIGSAG 98
 DB 10 VIGGKFKRLGSGSGSGELYLGINIQTEVAVKLEPVKTRHPOLQYESKITWFL-QGG 68
 QY 99 EGLPQVYVFGPCGKYNMAYELLGPSLEDFDCDRTFTLKTVMIAIQLLSRMEYVHSK 158
 DB 69 TGVPHLKMFPVEGEYSQWVIDLGPSEDFENCKRIFSLKSVMLADQLICREYVMSHR 128
 QY 159 NLIYRDYKPNFL--IGROGKKEVHTITDFGLAKETIDPETKRIPIREHKSLSGTAR 216
 DB 129 GFLHRDLPKPNFLMGLGRRANQ---YIIDYGLAKKPKDLOTKHIPRENKMLTGTAR 184
 QY 217 YMSINPHLGKESRRDLEALGHMEVFLRGSIPMOGLKADTLKERYQKIGDTRKNPPIE 276
 DB 185 YASVNHILGIEQSRDLESLGYLMFLRGSIPMOGLKAGTKQKQYDKISEKMLTSVE 244
 QY 277 ALCENPEEMATYLRVYRRLDFEKPDEYELRTFTDLFEKKGYPFDYAYDWV----- 329
 DB 245 TLCKSYDSEFTSYFHCRLRFEDKPDYSYLRRLFLREGYQLDYFDWTISKYPI 304
 QY 330 ---GRPIPTP-----VGSV-----HVDGASAITRES 353
 DB 305 GSSSRPRPPTPRPALDPPPPRAERAEKPTVGDLRGRTGAIETFRNVSOGALGDRSR 364
 QY 354 H-THRDSPSQOQPL-----RNOVYSTNGELNVDDPTGAHNAPIITA---HAEVEY 400
 DB 365 HRSDDLPSSAKVEHESRNGSTSKRGVISTRESSA-EPSENHSSKLFSSGSHHATTOR 423
 QY 401 VEEA 404
 DB 424 VPQS 427

Search completed: August 17, 2002, 20:17:39
 Job time: 3184 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 17, 2002, 20:16:35 ; Search time 24.7 Seconds

(without alignments)
661.524 Million cell updates/sec

Title: US-09-765-068-2

Perfect score: 2248
Sequence: 1 MDHPSREKDERQRTKPMQA.....EAKCCCFKRRKRTAQRHK 422

Scoring table: BLOSUM62
Gapop .10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	ID	Description
1	2248	100.0	422	KC11_HUMAN	Q9HCP0: Homo sapien
2	1915	85.2	390	KC11_RAT	Q62761: Rattus norv
3	1809	80.5	448	KC13_RAT	Q62763: Rattus norv
4	1783.5	79.3	447	KC13_HUMAN	Q9Y6M4: Homo sapien
5	1776.5	79.0	415	KC12_HUMAN	P78368: Homo sapien
6	1755	78.1	414	KC12_RAT	Q62762: Rattus norv
7	1313.5	58.4	276	KC13_BOVIN	P35509: Bos taurus
8	946.5	42.1	416	KC1E_MOUSE	P93674: Mus musculu
9	940.5	41.8	415	KC1E_MOUSE	Q9JMK2: Mus musculu
10	937	41.7	428	KC1D_HUMAN	P48730: Homo sapien
11	936	41.6	428	KC1D_RAT	Q06486: Rattus norv
12	924	41.1	365	HHP1_SCHPO	P40235: Schizosacch
13	924	41.1	439	KC13_SCHPO	Q74135: Schizosacch
14	922.5	41.0	435	KC12_SCHPO	P40234: Schizosacch
15	917	40.8	446	KC11_SCHPO	P40233: Schizosacch
16	907.5	40.4	400	HHP2_SCHPO	P40236: Schizosacch
17	886.5	39.9	535	RAG8_KULTA	P40220: Kluyveromyc
18	887.5	39.5	387	KC1D_ARATH	P42128: Arabidopsis
19	885.5	39.4	546	KC12_YEAST	P33292: Saccharomyc
20	884	39.3	538	KC11_YEAST	Q76324: Drosophila
21	877	39.0	538	KC11_YEAST	P43292: Saccharomyc
22	867	38.6	578	YMR1_CAEEL	Q20471: Caenorhabd
23	863.5	38.4	325	KC1A_RAT	P97633: Rattus norv
24	862.5	38.4	325	KC1A_BOVIN	P35506: Bos taurus
25	861.5	38.3	337	KC1A_CHICK	P71065: Gallus gall
26	861.5	38.3	324	KC1A_PLAIF4	P15726: Plasmodium
27	861.5	38.3	337	KC1A_HUMAN	P48729: Homo sapien
28	860.5	38.3	494	HR25_YEAST	P29285: Saccharomyc
29	820.5	36.5	337	KC1A_DROME	P54367: Drosophila
30	816	36.3	341	TKL1_CAEEL	P42163: Caenorhabd
31	800	35.6	524	CK13_YEAST	P39962: Saccharomyc
32	795.5	35.4	336	KC1B_BOVIN	P35507: Bos taurus
33	352.5	15.7	125	KC1A_PIG	O19175: Sus scrofa

ALIGNMENTS

RESULT	1	STANDARD	PRT	422 AA
KC11_HUMAN				
ID	KC11_HUMAN			
AC	Q9HCP0: Q9HCP1			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Casein kinase I, gamma 1 isoform (EC 2.7.1.-) (CKI-gamma 1).			
GN	CSNK1G1			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Kusuda J., Hirai M., Osada N., Hashimoto K.;			
RT	"Cloning, expression analysis and chromosomal mapping of human casein			
RT	kinase I gamma 1 (CSNK1G1): identification of two types of cDNA			
RT	encoding the kinase protein associated with heterologous			
RT	carboxy-terminal sequences."			
RL	Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.			
CC	-1- FUNCTION: CASEIN KINASES ARE OPERATIONALLY DEFINED BY THEIR			
CC	PREFERENTIAL UTILIZATION OF ACIDIC PROTEINS SUCH AS CASEINS			
CC	AS SUBSTRATES. IT CAN PHOSPHORYLATE A LARGE NUMBER OF PROTEINS.			
CC	-1- SUBUNIT: MONOMER (BY SIMILARITY).			
CC	-1- SUBCELLULAR LOCATION: Cytoplasmic.			
CC	-1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1L (SHOWN HERE) AND 1S; ARE			
CC	PRODUCED BY ALTERNATIVE SPLICING.			
CC	-1- PTM: AUTOPHOSPHORYLATED (BY SIMILARITY).			
CC	-1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.			
CC	CASEIN KINASE I SUBFAMILY.			
CC	-----			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@sib-sib.ch).			
CC	-----			
DR	EMBL; AB042563; BAB17839.1; -			P34516 caenorhabd
DR	EMBL; AB042562; BAB17838.1; -			P81123 oxycolaus
DR	MIM; 606274; -			P21098 vaccinia vi
DR	InterPro: IPR000719; Euk_pkinase.			P24362 vaccinia vi
DR	InterPro: IPR002290; Ser_thr.pkinase.			Q91523 fowlpox vir
DR	InterPro: IPR001245; Tyr_pkinase.			P16913 vaccinia vi
DR	Pfam; PF00069; pkinase.1.			P33800 variola vir
DR	SMART; SM00220; STKC; 1.			P20505 vaccinia vi
DR	SMART; SM00219; TYRKC; 1.			Q91509 fowlpox vir
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.			P42169 caenorhabd
DR	PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.			P49673 ascaris suu
DR	PROSITE; PS00108; PROTEIN_KINASE_ST; 1.			
DR	TRANSFERASE; Serine/threonine-protein kinase; ATP-binding;			
KW	Multi-enzyme family; Phosphorylation; Alternative splicing.			
FT	DOMAIN 44 315			
FT	NP_BIND 50 58			
FT	ATP (BY SIMILARITY).			

FT BINDING 73 73 ATP (BY SIMILARITY).
 FT ACT SITE 164 164 BY SIMILARITY.
 FT VARSPLIC 370 422 VVSSTGELNVDPTGASHNAPITAHAEVEVEAKCCCF
 FT KRKKTKAQRK -> SLRTYAEHYDVNNSAIHMRGRT
 FT (IN ISOBORN 15)
 SQ SEQUENCE 422 AA: 48511 MW: 8875922349897645 CRC64;

Query Match 100.0%; Score 2248; DB 1; Length 422;
 Best Local Similarity 100.0%; Pred. No. 8.7e-162;
 Matches 422; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDHPSREKDERQRTTKPMAORSACSRPSSSSSGVLMVGNPFRVGRKKIGCGNGEURL 60
 DB 1 MDHPSREKDERQRTTKPMAORSACSRPSSSSSGVLMVGNPFRVGRKKIGCGNGEURL 60
 QY 61 GKNLYTNEYVAIKLEPIKSRAPQHLERYFKQLGSAGEGLPQVYYPFGCGKYNAMVLEL 120
 DB 61 GKNLYTNEYVAIKLEPIKSRAPQHLERYFKQLGSAGEGLPQVYYPFGCGKYNAMVLEL 120
 QY 121 LGPSLEDFDLCDRFTFLTKYLMIAIQLSRMEYHSKNLYRDVKNPFLIGRGNKE 180
 DB 121 LGPSLEDFDLCDRFTFLTKYLMIAIQLSRMEYHSKNLYRDVKNPFLIGRGNKE 180
 QY 181 HVHIIDFGLAKEYIDPETKKHPIYREKSLTGTAARYMSINTHLGKESRRDDLEALGHM 240
 DB 181 HVHIIDFGLAKEYIDPETKKHPIYREKSLTGTAARYMSINTHLGKESRRDDLEALGHM 240
 QY 241 FMYFLRGSLEPMOGLKADTLKERYOKIGDTKNTPIEALCENFPEMAATYLRVRLDFFE 300
 DB 241 FMYFLRGSLEPMOGLKADTLKERYOKIGDTKNTPIEALCENFPEMAATYLRVRLDFFE 300
 QY 301 KPDEYELTLETFDLEFEKGYTFDYADWVGRPIPTVGSVHVDGASAIRESHTHRDRP 360
 DB 301 KPDEYELTLETFDLEFEKGYTFDYADWVGRPIPTVGSVHVDGASAIRESHTHRDRP 360
 QY 361 SQOQPLRNQVVSSTNGELNVDPTGASHNAPITAHAEVEVEAKCCCFKRKKTKAQR 420
 DB 361 SQOQPLRNQVVSSTNGELNVDPTGASHNAPITAHAEVEVEAKCCCFKRKKTKAQR 420
 QY 421 HK 422
 DB 421 HK 422

RESULT 2

KC13_RAT STANDARD; PRT; 390 AA.
 AC Q62761;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Casein kinase I, gamma 1 isoform (EC 2.7.1.-) (CKI-gamma 1).
 GN CSNK1G1.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 OX NCBI_Taxid=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RX MEDLINE=95279411; PubMed=7759525;
 RA Zhai L., Graves P.R., Robinson L.C., Italiano M., Culbertson M.R.,
 RA Rowles J., Cobb M.H., Depauli-Roach A.A., Roach P.J.;
 RT "Casein kinase I gamma subfamily. Molecular cloning, expression, and
 RT characterization of three mammalian isoforms and complementation of
 RT defects in the Saccharomyces cerevisiae YCK genes.";
 RL J. Biol. Chem. 270:12171-12174(1995).
 CC -1- FUNCTION: CASEIN KINASES ARE OPERATIONALLY DEFINED BY THEIR
 CC PREFERENTIAL UTILIZATION OF ACIDIC PROTEINS SUCH AS CASEINS
 CC AS SUBSTRATES. IT CAN PHOSPHORYLATE A LARGE NUMBER OF PROTEINS.
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.

CC -1- PTM: AUTOPHOSPHORYLATED.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC CASEIN KINASE I SUBFAMILY.

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 CC -----

DR EMBL: U22296; AAC52200.1; -;
 DR HSSP: Q06486; 1CKI.
 DR InterPro: IPR000719; Euk_Pkinase.
 DR InterPro: IPR002290; Ser_thr_Pkinase.
 DR Pfam: PF00069; Pkinase; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 KW Transferase; Serine/threonine-protein kinase; ATP-binding;
 KW Multigene family; Phosphorylation.
 FT DOMAIN 44 315 PROTEIN KINASE.
 FT NP_BIND 50 58 ATP (BY SIMILARITY).
 FT BINDING 73 73 ATP (BY SIMILARITY).
 FT ACT_SITE 164 164 BY SIMILARITY.
 SQ SEQUENCE 390 AA: 45126 MW: 88985952240762 CRC64;

Query Match 85.2%; Score 1915; DB 1; Length 390;
 Best Local Similarity 96.0%; Pred. No. 8.4e-137;
 Matches 359; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 MDHPSREKDERQRTTKPMAORSACSRPSSSSSGVLMVGNPFRVGRKKIGCGNGEURL 60
 DB 1 MDHPSREKDERQRTTKPMAORSACSRPSSSSSGVLMVGNPFRVGRKKIGCGNGEURL 60
 QY 61 GKNLYTNEYVAIKLEPIKSRAPQHLERYFKQLGSAGEGLPQVYYPFGCGKYNAMVLEL 120
 DB 61 GKNLYTNEYVAIKLEPIKSRAPQHLERYFKQLGSAGEGLPQVYYPFGCGKYNAMVLEL 120
 QY 121 LGPSLEDFDLCDRFTFLTKYLMIAIQLSRMEYHSKNLYRDVKNPFLIGRGNKE 180
 DB 121 LGPSLEDFDLCDRFTFLTKYLMIAIQLSRMEYHSKNLYRDVKNPFLIGRGNKE 180
 QY 181 HVHIIDFGLAKEYIDPETKKHPIYREKSLTGTAARYMSINTHLGKESRRDDLEALGHM 240
 DB 181 HVHIIDFGLAKEYIDPETKKHPIYREKSLTGTAARYMSINTHLGKESRRDDLEALGHM 240
 QY 241 FMYFLRGSLEPMOGLKADTLKERYOKIGDTKNTPIEALCENFPEMAATYLRVRLDFFE 300
 DB 241 FMYFLRGSLEPMOGLKADTLKERYOKIGDTKNTPIEALCENFPEMAATYLRVRLDFFE 300
 QY 301 KPDEYELTLETFDLEFEKGYTFDYADWVGRPIPTVGSVHVDGASAIRESHTHRDRP 360
 DB 301 KPDEYELTLETFDLEFEKGYTFDYADWVGRPIPTVGSVHVDGASAIRESHTHRDRP 360
 QY 361 SQOQPLRNQVVSST 374
 DB 361 SQOQPLRNQVVSST 374

RESULT 3

KC13_RAT STANDARD; PRT; 448 AA.
 AC Q62763;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Casein kinase I, gamma 3 isoform (EC 2.7.1.-) (CKI-gamma 3).
 GN CSNK1G3.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Query	Match	79.3%	Score 1783.5	DB 1	Length 447
Db	298	EXPYDYLARKLEFTDLPDRKGMFDEYEDYMWIGKQLPTPYGAVQGDPALSS-NREAQHNDK	356		
Qy	360	-----PSCQ-----QPLRN-----QVYSTNGELINDDPFGAHSNA	390		
Db	357	IQOSKMSADHRAAMDSCQANPHHRLAALADRHGSGVYVSSVTNGELINTDDPTAGRSNA	416		
Qy	391	PITAAHEVYVEEPAKCCCEFFKRKRKKTQNRK	422		
Db	417	PITAFTEVYEMDETKCCCFEKKRKRKKTQNRK	448		
RESULT	4				
KL13_HUMAN					
AC	Q9Y6M4	Q9Y6M3	STANDARD; PRT; 447 AA.		
DT	30-MAY-2000	(Rel. 39, Created)			
DT	30-MAY-2000	(Rel. 39, Last sequence update)			
DT	16-OCT-2001	(Rel. 40, Last annotation update)			
DE	Caskein kinase I, gamma 3 isoform (EC 2.7.1.-) (CRT-gamma 3).				
GN	CSNK1G3.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RA	SEQUENCE FROM N.A.				
RT	TISSUE=Testis;				
RX	MEDLINE=99126346; PubMed=9925945;				
RA	Kinase J., Hirai M., Toyoda A., Tanuma R., Hashimoto K.;				
RT	*Cloning and chromosome mapping of the human caskein kinase I gamma3 gene (CSNK1G3).;				
RL	Cytogenet. Cell Genet. 83:101-103(1998).				
CC	-1- FUNCTION: CASEIN KINASES ARE OPERATIONALLY DEFINED BY THEIR PREFERENTIAL UTILIZATION OF ACIDIC PROTEINS SUCH AS CASEINS AS SUBSTRATES. IT CAN PHOSPHORYLATE A LARGE NUMBER OF PROTEINS.				
CC	-1- SUBUNIT: MONOMER (BY SIMILARITY).				
CC	-1- SUBCELLULAR LOCATION: Cytoplasm;c.				
CC	-1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 3 (SHOWN HERE) AND 3L/CSNK1G3L; ARE PRODUCED BY ALTERNATIVE SPLICING.				
CC	-1- PTM: AUTOPHOSPHORYLATED (BY SIMILARITY).				
CC	-1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. CASEIN KINASE I SUBFAMILY.				
CC	-----				
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CC	-----				
DR	EMBL: AF049089; AAD26525.1; -.				
DR	EMBL: AF049090; AAD26526.1; -.				
DR	HSSP: P40233; ICSN.				
DR	MM: 604253; -.				
DR	Interpro: IPR000719; Euk_pkinase.				
DR	Interpro: IPR002290; Ser_thr_pkinase.				
DR	Pfam: PF00069; pkinase.1.				
DR	PROSITE: PS00107; PROTEIN_KINASE_ATP.1.				
DR	PROSITE: PS00108; PROTEIN_KINASE_ST.1.				
KW	PROSTATE; PS50011; PROTEIN_KINASE_DOM.1.				
KW	Transferrase; Serine/threonine-protein kinase; ATP-binding;				
KW	MultiGene family; Phosphorylation; Alternative splicing.				
FT	DOMAIN 43 313				
FT	NP-BIND 49 57				
FT	ACT_SITE 72 72				
FT	ACT_SITE 162 162				
FT	VARSPIC 430 430				
QO	SEQUENCE 447 AA; 51501 MW; CFB9A16BFED06BDC CRC64;				

Best Local Similarity 76.8%; Pred. No. 7.6e-127;
Matches 347; Conservative 30; Mismatches 40; Indels 35; Gaps 8;

```

QY 1 MDHSEKDER-QRTTKPMAORSAHCRSPSSSSSGVLMGPNFRVKGKIGCNFGLR 59
  1 MENKKKDDKDDMAR-SGRSGHNRGTG-SSSSGLVMGPNFRVKGKIGCNFGLR 58
QY 60 LGKMLTYNEVAIKLEPIKSRAPOLHLEFRYKOLGSGEGLPVYFFGPCGTANYLE 119
  59 LGKMLTYNEVAIKLEPIKSRAPOLHLEFRYKOLGSGEGLPVYFFGPCGTANYLE 117
QY 120 LLSGLELFDLCRTFTLTKVLMIAIOLLSRMEVHSHKNLIYDVYPENFLIGROGKK 179
  118 LLSGLELFDLCRTFTLTKVLMIAIOLLSRMEVHSHKNLIYDVYPENFLIGRPRKT 177
QY 180 EHVHIIDFGLAKETIDPETKHHIPYREHKSITGTARMSINTHLGKQSRDLEALGH 239
  178 QOVHIIDFGLAKETIDPETKHHIPYREHKSITGTARMSINTHLGKQSRDLEALGH 237
QY 240 MFMVFLRSLPWOGLKADTLKERYOKIGDTRKNTPIEALCENPEEMATYLRVYRLDFE 299
  238 MFMVFLRSLPWOGLKADTLKERYOKIGDTRKNTPIEALCENPEEMATYLRVYRLDFE 296
QY 300 EKPRYEYLRKFTLPEKKGTYTAYDWRPPTPYGSHVDSGASATRESHTHRD 359
  297 EKPRYEYLRKFTLPEKKGTYTAYDWRPPTPYGSHVDSGASATRESHTHRD 355
QY 360 PSCOO-----PLRN-----QVYSSINGELVDDPTGAHSA 390
  356 MOGSKNSADHRAAMDQANPHHLRAHLADRGGSGVQVYSSINGELVDDPTGAHSA 415
QY 391 PITAAEVEVEAEKCCCFKRRKRKTAQRHK 422
  416 PITAPTEVEVDETKCCCFKRRKRKTIQRHK 447

```

RESULT 5
KC12_HUMAN STANDARD; PRT; 415 AA.

AC P78368; 000704;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Casein kinase I, gamma 2 isoform (EC 2.7.1.-) (CKI-gamma 2).
GN CSNK1G2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE-Testis;
RC MDLINE=98066772; Pubmed=9403068;
RA Kitabayashi A.N., Kusuda J., Hirai M., Hashimoto K.;
RT Cloning and chromosomal mapping of human casein kinase I gamma 2
RT (CSNK1G2)."
RL Genomics 46:133-137(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA Lamerzin J.E., McCreedy P.M., Skowronski E., Adamson A.M.,
RA Burkhardt-Schultz K., Gordon L., Kyle A., Ramirez M., Stiliwgen S.,
RA Phan H., Velasco N., Do L., Regala W., Terry A., Ganes J.,
RA Danganan L., Poundstone P., Christensen M., Georgescu A., Avila J.,
RA Liu S., Attix C., Andreise T., Traankheim M., Amico-Keller G.,
RA Coefield J., Duarte S., Lucas S., Bruce R., Thomas P., Quan G.,
RA Krommiller B., Arellano A., Montgomery M., Ow D., Nolan M., Trong S.,
RA Kobayashi A., Olsen A.S., Carraro A.V.,
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases
CC -1- FUNCTION: CASEIN KINASES ARE OPERATIONALLY DEFINED BY THEIR
CC PREFERENTIAL UTILIZATION OF ACIDIC PROTEINS SUCH AS CASEINS
CC AS SUBSTRATES. IT CAN PHOSPHORYLATE A LARGE NUMBER OF PROTEINS.
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.

```

CC -1- TISSUE SPECIFICITY: TESTIS.
CC -1- PTM: AUTOPHOSPHORYLATED (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CASEIN KINASE I SUBFAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U89896; AAB8627.1; -.
CC EMBL; AF001177; AAC00212.1; -.
CC EMBL; AC005306; AAC26983.1; -.
CC HSSP; 006486; 1CKI.
CC MIM; 602214; -.
CC InterPro; IPR007719; Euk_pkinase.
CC InterPro; IPR002290; Ser_thr_pkinase.
CC Pfam; PF00069; pkinase; 1.
CC PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
CC PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
CC PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
CC Transferrase; Serine/threonine-protein kinase; ATP-binding;
CC Multigene family; Phosphorylation.
CC DOMAIN
CC NP_BIND 52 60 ATP (BY SIMILARITY).
CC FT BIND 75 75 ATP (BY SIMILARITY).
CC FT ACT_SITE 165 165 BY SIMILARITY.
CC FT ACT_SITE 165 165 BY SIMILARITY.
CC SQ SEQUENCE 415 AA; 47457 MW; 036A39148A1DA038 CRC64;

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Query Match 79.0%; Score 1776.5; DB 1; Length 415;
Best Local Similarity 80.0%; Pred. No. 2.3e-126;
Matches 333; Conservative 31; Mismatches 41; Indels 11; Gaps 3;

```

QY 7 EKDERQRTTKPMAORSAHCRSPSSSSSGVLMGPNFRVKGKIGCNFGLR 66
  11 ETEGRMRMSKAGGSSHGIRSSG--TSSGLVMGPNFRVKGKIGCNFGLR 68
QY 67 NEVAIKLEPIKSRAPOLHLEFRYKOLGSGEGLPVYFFGPCGTANYLELSPSLE 126
  69 NEVAIKLEPIKSRAPOLHLEFRYKOL-SATSEGVPOVYFFGPCGTANYLELSPSLE 127
QY 127 DLFDLCRTFTLTKVLMIAIOLLSRMEVHSHKNLIYDVYPENFLIGROGKKEHYHII 186
  128 DLFDLCRTFTLTKVLMIAIOLLSRMEVHSHKNLIYDVYPENFLIGROGKKEHYHII 187
QY 187 DFLAKETIDPETKHHIPYREHKSITGTARMSINTHLGKQSRDLEALGHMFTFLR 246
  188 DFLAKETIDPETKHHIPYREHKSITGTARMSINTHLGKQSRDLEALGHMFTFLR 247
QY 247 GSILPWOGLKADTLKERYOKIGDTRKNTPIEALCENPEEMATYLRVYRLDFEKPXYE 306
  248 GSILPWOGLKADTLKERYOKIGDTRKNTPIEALCENPEEMATYLRVYRLDFEKPXYE 307
QY 307 LRTLFTLPEKKGTYTAYDWRPPTPYGSHVDSGASATRESHTHRDPSQQPL 366
  308 LRTLFTLPEKKGTYTAYDWRPPTPYGSHVDSGASATRESHTHRDPSQQPL 365
QY 367 RNQVYSSINGELVDDPTGAHSAHPITAAEVEVEAEKCCCFKRRKRKTAQRHK 422
  360 RNQVYSSINGELVDDPTGAHSAHPITAAEVEVEAEKCCCFKRRKRKTAQRHK 415

```

RESULT 6
KC12_RAT STANDARD; PRT; 414 AA.

AC Q62762;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)

[illegible]

Query Match	41.8%	Score 940.5	DB 1	Length 416
Best Local Similarity	51.1%	Pred. No. 1.6e-63		
Matches 180	Conservative 68	Mismatches 89	Indels 15	Gaps 3
38	LMVGNFRVGGKIGGNGELRLGNLTNEVAKLEPIKRAPQDHLHFYFQDLSA	97		

[illegible]

DR EMBL; U29171; AAC50807.1; -.
DR EMBL; U31285; AAC50808.1; -.
DR EMBL; BC003558; AAH03558.1; -.
DR HSSP; Q06486; 1CKJ.
DR MIM; 600864; -.
DR InterPro; IPR000719; Euk_Pkinase.

DB 347 TPTSHANTSPRPVSGME-----REKRVSMRLHR 375

RESULT 12

ID HRP1_SCHPO STANDARD; PRT; 365 AA.

AC P40235;

DT 01-FEB-1995 (Rel. 31, Created)

DT 01-FEB-1995 (Rel. 31, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Casein kinase I homolog hnp1 (EC 2.7.1.-).

GN HRP1 OR SPBC3H7.15.

OS Schizosaccharomyces pombe (fission yeast).

OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;

OC Schizosaccharomycetales; Schizosaccharomycetaceae;

OC Schizosaccharomycetes.

OX NCBI_TaxID=4896;

RP SEQUENCE FROM N.A.

RC STRAIN=SP66;

RA MEDLINE=94354807; PubMed=8074660;

RT Keatney P., Ebert M., Kuret J.;

RT "Molecular cloning and sequence analysis of two novel fission yeast

RT casein kinase-1 isoforms.";

RL Biochem. Biophys. Res. Commun. 203:231-236(1994).

RP SEQUENCE FROM N.A.

RC MEDLINE=94298768; PubMed=8026462;

RA Dhillon N., Hoekstra M.F.;

RT "Characterization of two protein kinases from Schizosaccharomycetes

RT pombe involved in the regulation of DNA repair.";

RL EMO J. 13:2777-2788(1994).

RP SEQUENCE FROM N.A.

RC STRAIN=972;

RA Lyne M., Rajandream M.A., Barrell B.G., Jimenez Martinez J.;

RT Submitted (Aug-1998) to the EMBL/Genbank/DBJ databases.

CC -1- FUNCTION: INVOLVED IN DNA REPAIR. HAS A PROBABLE ROLE IN REPAIRING

CC ACTIVATED DNA AND MAY REGULATE THE ACTIVITY OF PROTEIN(S) INVOLVED

CC IN DOUBLE STRAND BREAK REPAIR CAUSED BY GAMMA RAYS.

CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).

CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

CC CASEIN KINASE I SUBFAMILY.

CC -----

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CC -----

DR EMBL; U10863; AAA21544.1; -

DR EMBL; X78871; CAA55473.1; -

DR EMBL; AL031261; CAA20311.1; -

DR PIR; S44196; S44196.

DR HSSP; Q06486; ICKT.

DR InterPro; IPR000719; Euk_kinase.

DR InterPro; IPR002290; Ser_thr_kinase.

DR Pfam; PF00069; kinase.1.

DR PROSITE; PS00107; PROTEIN_KINASE_ATP.1.

DR PROSITE; PS00108; PROTEIN_KINASE_ST.1.

DR PROSITE; PS50011; PROTEIN_KINASE_DOM.1.

KW transferase; Serine/threonine-protein kinase; ATP-binding; DNA repair;

KW Nuclear protein.

FT DOMAIN 11 279

FT NP_BIND 17 25

FT BINDING 40 40

FT ACT_SITE 130 130

FT DOMAIN 289 323

FT SEQUENCE 365 AA; 42450 MW; D637C950555F1339 CRC64;

Query Match 41.18; Score 924; DB 1; Length 365;
Best Local Similarity 49.28; Pred. No. 2,3e-62;
Matches 190; Conservative 63; Mismatches 75; Indels 58; Gaps 9;

QY 38 LMGPNFVGVKKIGGNGELRLGNLTNEVAIKLEPISRAPOLHEVRYQLGSA 97

DB 5 LRGKRYRIGRRKIGSGSFGDYLGNVSGEVAIKLESTRKHPQLEYERVYIL-SG 63

QY 98 GEGLEQVYVFPFGCKYNNAMVELLGPSPLEDFDLCDRTFTLTKVLMIAIQLSRMEYVHS 157

DB 64 GVGIFPVNMFVECDYNNAMVDLPSPLEDFLPCNRRFSKTVLLADQLISREFIHS 123

QY 158 KNLIVRDYKPNFL-IGRGKKKEVHIIDFLAKXYIDPEYKHHIYREHKSITGTA 215

DB 124 KSLFHRDKPQNFMLGKIRGNG---VNIIDFLAKYRDKHKLHIYREHKNLTGTA 179

QY 216 RYMSINTHLGKQSRDLEALGHFMFPLRSLPWQGLKADTLKEROKIGDTKRNPI 275

DB 180 RYASINTHLGIEQSRDLESLGYLVYFCRSLPWQGLKATKOKYKIKERKISTPT 239

QY 276 EALCENFPEEMATYLRVYRRLDFEFKPDYEVYRTLTFTLFEKGYTFPVDWGRPIPT 335

DB 240 EYLCGFQFQESTYINTRSLRFDKPDYATYRKLFRLDFCRQSYEPDYMFW----- 292

QY 336 PVGSVYVDSGASATRESHTHRDPSQO-----PLRN---QVSS 373

DB 293 -----TLKRRTOQDQHOQLOQLSATFOAINPPERSFRNYOKQNFDE 338

QY 374 TNGELN-----VDDP--TGA-HSNAP 391

DB 339 KGDINTVTPVINDPSATGAOYINRP 364

RESULT 13

ID CK13_SCHPO STANDARD; PRT; 439 AA.

AC Q74135;

DT 15-JUL-1999 (Rel. 38, Created)

DT 15-JUL-1999 (Rel. 38, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Casein kinase I homolog ck13 (EC 2.7.1.-).

GN CK13 OR SPAC1805.05.

OS Schizosaccharomyces pombe (fission yeast).

OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;

OC Schizosaccharomycetales; Schizosaccharomycetaceae;

OC Schizosaccharomycetes.

OX NCBI_TaxID=4896;

RP SEQUENCE FROM N.A.

RC MEDLINE=98322261; PubMed=9651503;

RA Kitamura K., Yamashita I.;

RT "Identification of a novel casein kinase-1 homolog in fission yeast

RT Schizosaccharomyces pombe.";

RL Gene 214:131-137(1998).

RP SEQUENCE FROM N.A.

RC STRAIN=972;

RA Rieger M., McDougall R.C., Rajandream M.A., Barrell B.G.;

RT Submitted (Sep-1999) to the EMBL/Genbank/DBJ databases.

CC -1- FUNCTION: CASEIN KINASES ARE OPERATIONALLY DEFINED BY THEIR

CC PREFERENTIAL UTILIZATION OF ACIDIC PROTEINS SUCH AS CASEINS

CC AS SUBSTRATES.

CC -1- SUBCELLULAR LOCATION: Cytoplasmic.

CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

CC CASEIN KINASE I SUBFAMILY.

CC -----

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CC EMBL: AB010643; BAA32482.1; -
 DR EMBL: AL117390; CAB5846.1; -
 DR HSSP: P40233; ICSN.
 DR InterPro: IPR000719; Euk_Pkinase.
 DR InterPro: IPR002290; Ser_thr_Pkinase.
 DR Pfam: PF00069; Pkinase.1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP.1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST.1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM.1.
 KM Transferase: Serine/threonine-protein kinase; ATP-binding.
 FT DOMAIN 15 286 PROTEIN KINASE.
 FT NP_BIND 21 29 ATP (BY SIMILARITY).
 FT BINDING 44 44 ATP (BY SIMILARITY).
 FT ACT_SITE 134 134 BY SIMILARITY.
 FT DOMAIN 376 382 POLY-GLN.
 FT DOMAIN 387 392 POLY-GLN.
 SO SEQUENCE 439 AA; 50215 MW; CE6A1B1C1A8A8F6 CMC64;

Query Match 41.1%; Score 924; DB 1; Length 439;
 Best Local Similarity 46.1%; Pred. No. 3e-62;
 Matches 196; Conservative 63; Mismatches 126; Indels 40; Gaps 6;

QY 31 SSSSSGLVMPNFRVGGKIKCGNFGELRLKNTNYVAIKLEPIKSRAPQHLERYF 90
 2 STSSHNVGVYRVGKIKGEGSGMLFGVNLINOPALKEFSRSEVPOLRDEYLT 61
 QY 91 YKOGSAGEGLPOVYFGCGKYNAMVELLGPSELEDFDCDRFTLTQVLMIAIOLLS 150
 62 YKLMGL-PGIPSYTYGGEMNLVMDLGPSELEDFDCGRFSKTYAMAKKQIT 120
 QY 151 RMEVYHKNLIRVDKKNFLIGROGKKEVHIHIDGLAKKEYIDPEKTHIPREHKS 210
 121 RIQSVHERHFIYRDIKPDNFIIGPGSKTENVIYAVDGMKQYRDXPHVHRYNEKS 180
 QY 211 LTGARVMSINTHLGKESRDDEALGHNMYFLRGLPMOGLKADTLKRYOKIGDTK 270
 181 LSGARVMSINTHLGKESRDDEALGHNMYFLRGLPMOGLKAAKNKRYEYIGTK 240
 QY 271 RNTGTEALCENPEPMATYLRVRLDFEKEPDYEYLTFTDLEFKKGYEDVAYDMV- 329
 241 QVTLKELCEGYKPEFLQYMIYARNLGEAPDYLRSLDSLLRLNETDDGKYDWT 300
 QY 330 --GRPIPTPVGSYVH-----DSGASAITRESHTHD---RSQOQPLRNQVSS 373
 301 LNNKGWQVSAKQHVQRRHTQGTNNRQSTIPPYATRONLLSPSKQTPVNNVVDAS 360
 QY 374 T-----NGLNVDDPTGAHSNAPITAH-AEVEVVEAKCCCFK 411
 361 VATQKDGIPGKAASPOVQOQOOTSAAQOQOPQVEOPAPOTPTOPVDTQAAKAPAPSE 420
 QY 412 RKRRK 416
 DB 421 KSRKK 425

RESULT 14
 CK12_SCHPO
 ID CK12_SCHPO STANDARD; PRT; 435 AA.
 AC P40234; O9P798;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Casein kinase I homolog ck12 (EC 2.7.1.-).
 GN CK12 OR SPB35G2.05C.
 OS Schizosaccharomyces pombe (fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN-SP66;
 RA MEDLINE-94216312; PubMed-8163505;
 RA Wang P.-C., Vancura A., Desai A., Carmel G., Kuret J.;
 RT "Cytoplasmic forms of fission yeast casein kinase-1 associate
 primarily with the particulate fraction of the cell.";
 RL J. Biol. Chem. 269:12014-12023(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-972;
 RA Seeger K., Harris D., Wood V., Rajandream M.A., Barrell B.G.,
 RA Mccombie W.R.;
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: CASEIN KINASES ARE OPERATIONALLY DEFINED BY THEIR
 CC PREFERENTIAL UTILIZATION OF ACIDIC PROTEINS SUCH AS CASEINS
 CC AS SUBSTRATES. CK12 MAY CONTRIBUTE TO THE REGULATION OF
 CC MORPHOLOGY.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC CASEIN KINASE I SUBFAMILY.

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 CC
 DR EMBL: D06930; AAA19020.1; -
 DR EMBL: AL163702; CAB87367.1; -
 DR HSSP: P40233; ICSN.
 DR InterPro: IPR000719; Euk_Pkinase.
 DR InterPro: IPR002290; Ser_thr_Pkinase.
 DR InterPro: IPR001245; Tyr_Pkinase.
 DR Pfam: PF00069; Pkinase.1.
 DR SMART: SM00220; S_TKc; 1.
 DR SMART: SM00219; TYKc; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP.1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST.1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM.1.
 KM Transferase: Serine/threonine-protein kinase; ATP-binding.
 FT DOMAIN 12 282 PROTEIN KINASE.
 FT NP_BIND 18 26 ATP (BY SIMILARITY).
 FT BINDING 41 41 ATP (BY SIMILARITY).
 FT ACT_SITE 131 131 BY SIMILARITY.
 FT CONFLICT 169 169 H -> Y (IN REF. 1).
 SO SEQUENCE 435 AA; 49746 MW; 74CA7F1001B31F34 CRC64;

Query Match 41.0%; Score 922.5; DB 1; Length 435;
 Best Local Similarity 58.2%; Pred. No. 3.e-62;
 Matches 173; Conservative 53; Mismatches 68; Indels 3; Gaps 2;

QY 34 SSSGLVMPNFRVGGKIKCGNFGELRLKNTNYVAIKLEPIKSRAPQHLERYF 93
 2 NSQTSVGVYRVGKIKGEGSGVIFDGMNLNOLAIKEPKSEKPEPOLRDEYRKL 61
 QY 94 L-GSAGEGLPOVYFGCGKYNAMVELLGPSELEDFDCDRFTLTQVLMIAIOLLSRM 152
 62 LVGNA--GIPVYTYFGGGLNLIIVIDLGSLEDFEWCGRRSVTVAMTAQOMLSRV 119
 QY 153 EYVHKNLIRVDKKNFLIGROGKKEVHIHIDGLAKKEYIDPEKTHIPREHKS 212
 120 QTIHEKNLIVYDIKPDNFIIGPSRRNANMYVDFGAKYRDPKTKOHIPYSEKSL 179
 QY 213 GTARYMSINTHLGKESRDDEALGHNMYFLRGLPMOGLKADTLKERYOKIGDKN 272
 180 GTARYMSINTHLGKESRDDEALGHNMYFLRGLPMOGLKAAKNKRYEYIGTK 239
 QY 273 TPTEALCENPEPMATYLRVRLDFEKEPDYEYLTFTDLEFKKGYEDVAYDMV 329
 240 TSISELCAGFPNERSKMTYVRSLEFDEPDYARLQELFDVLANADINDGYVDM 296

```

RESULT 15
ID CKII_SCHPO STANDARD: PRT: 446 AA.
AC P40233; Q9UDL9;
DT 01-FEB-1995 (Rel. 31, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Casein kinase I homolog ck11 (EC 2.7.1.-).
GN CK11 OR SPBC1347.06C.
OS Schizosaccharomyces pombe (fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OC NCBI_taxid=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SP66;
RX MEDLINE-94216312; PubMed-8163505;
RA Wang P.-C., Vancura A., Desai A., Carmel G., Kuret J.;
RT "Cytoplasmic forms of fission yeast casein kinase-1 associate
RT primarily with the particulate fraction of the cell.";
RL J. Biol. Chem. 269:12014-12023(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-972;
RA Wood V., Rajandream M.A., Barrell B.G., Rieger M.;
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RX X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 1-298.
RX MEDLINE-95196745; PubMed-7889932;
RA Xu R.-M., Carmel G., Sweet R.M., Kuret J., Cheng X.;
RT "Crystal structure of casein kinase-1, a phosphate-directed protein
RT kinase.";
RL EMBO J. 14:1015-1023(1995).
CC -1- FUNCTION: CASEIN KINASES ARE OPERATIONALLY DEFINED BY THEIR
CC PREFERENTIAL UTILIZATION OF ACIDIC PROTEINS SUCH AS CASEINS
CC AS SUBSTRATES.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CASEIN KINASE I SUBFAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U06929; AAA19019.1; -.
DR EMBL: AL035346; CAB37437.1; -.
DR PDB: 1CSN; 31-JUL-95.
DR PDB: 2CSN; 08-MAR-96.
DR InterPro: IPR000719; Ser_thr_kinase.
DR InterPro: IPR002290; Ser_thr_kinase.
DR Pfam: PF00069; Kinase; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP_1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST_1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM_1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding;
KW 3D-structure.
FT DOMAIN 12 274 PROTEIN KINASE.
FT NP_BIND 18 26 ATP.
FT BINDING 41 41 ATP.
FT ACT_SITE 131 131
FT ACT_SITE 82 82
FT CONFLICT 310 310 R -> V (IN REF. 1).
FT CONFLICT 310 310 R -> Q (IN REF. 1).
SQ SEQUENCE 446 AA; 50424 MW; D813483056D8FD8 CRC64;

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Query Match 40.8%; Score 917; DB 1; Length 446;
Best Local Similarity 45.5%; Pred. No. 1e-61;

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Matches 188; Conservative 69; Mismatches 102; Indels 54; Gaps 9;
QY 39 MGCPRFRYCKKIGCGNFGELRLGKMLYTEVEYAIKLEPIKSRAPOLHLEFRYKOGSAG 98
   :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 7 VGVGHYKVRRIEGESFGVIFEGTNLNNQVAIKFEPRSDAPOLRDEYRTYKLLAGC- 65
QY 99 ECLPQVYFFGPCGKYNNAMVLELIGPSLEDLPDLCRTFTLTKVLMIAIQLSRMEYVHSK 158
   ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 66 TGIPRVYVYFGQGLNINILVIDLIGPSLEDLDDCGSKFVKTVANAKQMLARVQSIHEK 125
QY 159 NLIYDVKPENFLIGRGKKEHVHIIDFGLAKKEYIDETKHHIDYRDKSLTGARYM 218
   :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 126 SLVYRDIKPDNPLIGRPNKNNMIYVDFGWKFEYRDPVTKOHIPIREKKNLSGTARYM 185
QY 219 SINTHLGKQSRDDEALGKHMFWELRGSLPMOGIKADTLKERVOKIGDTKRNPIEAL 278
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 186 SINTHLGKQSRDDEALGKHMFWELRGSLPMOGIKADTLKERVOKIGDTKRNPIEAL 245
QY 279 CENPFEEMATYLRVYRRLDFFPEKPDYEVLRITLFTDLFEKKGYTFDYAYDW----- 328
   |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 246 CAGFPPEEFYKMYHARNLAFDAPDYDIQGLFSKYLERLNTEDENFDMNLLNKGKMG 305
QY 329 -----VGRPIPTPVGSVHVDGASAITRESHTHR-----DRP----- 360
   :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 306 SLKSRNAETENORSSKP-PAP-----KLESKSPALONHASTQVNVSKRSDYERPFAPHLN 360
QY 361 ----SQOQPLRNVY----VSTNGELNVDDPTGAHNSN--APITAH--AEVYVEE 403
   :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 361 SASDSAEAPNQNLSLPNPPTETKATTTVPDRSGLATQAPAPVADVHDSSEERYTRE 413

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Search completed: August 17, 2002, 20:23:54
Job time: 439 sec

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OY 67 NEVYAIKLEPIKSRAPOLHLEYRYKOLGSAG-----EG 100
DB 69 NEVYAIKLEPIKSRAPOLHLEYRYKOLSTGEADSGCPALLGOOMLRTSPMDVSFAEG 128
OY 101 LPQVYFPGCGKYNMVELLGPSSLEDFLDCDRTFTLKTVMIAIQLLSRMEYVHSKUL 160
DB 129 VPQVYFPGCGKYNMVELLGPSSLEDFLDCDRTFTLKTVMIAIQLLSRMEYVHSKUL 188
OY 161 IYRDVKNPEFLIGROGKKNKHVHIIIDGLAKEXIDPEPKKIPREKHSLSGTARYMSI 220
DB 189 IYRDVKNPEFLIGROGKKNKHVHIIIDGLAKEXIDPEPKKIPREKHSLSGTARYMSI 248
OY 221 NTHLKEOSRRDDLEALGHMFYFLRSGSLPMOGLKADTLKEXYKIGDKRATPIEVLCE 280
DB 249 NTHLKEOSRRDDLEALGHMFYFLRSGSLPMOGLKADTLKEXYKIGDKRATPIEVLCE 308
OY 281 NEPEMATYLVRYRLDPEFKPDYELRTLTDFEKKGYTDFYAVDWYGRIPPPVGSV 340
DB 309 SPEEMATYLVRYRLDPEFKPDYELRTLTDFEKKGYTDFYAVDWYGRIPPPVGSV 368
OY 341 HVDASASAITRESHTNRDRPSQOOLRNQVYSTNGELNVDPGTGASHNAPITAHAEVY 400
DB 369 HPD-----VPSQPHRDK--ALHTKNQALNSTNGELNVDPGTGASHNAPITAHAEVY 420
OY 401 VEEAKCCFRRKRRKKTQRHK 422
DB 421 ADETKCCFRRKRRKKSJDRHK 442

RESULT 2
OY 096AE9 PRELIMINARY: PRT: 307 AA.
ID 096AE9
OY 096AE9 01-DEC-2001 (TREMBLrel. 19, Created)
DB 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
OY 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DB CASEIN KINASE 1, GAMMA 1.
OY Homo sapiens (Human).
DB Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OY Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
DB NCBI_TaxID=9606;
OY 11
DB SEQUENCE FROM N. A.
OY RC TISSUE=MUSCLE. AND RHABDOMYOSARCOMA;
DB Strausberg R.;
OY Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DB EMBL; BC017236; AAH17236.1; -.
OY KM
DB KINASE.
OY SEQUENCE 307 AA; 35701 MW; 9C45DD47CB473186 CRC64;

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Query Match 72.6%; Score 1632; DB 4; Length 307;
 Best Local Similarity 100.0%; Pred. No. 4,6e-134;
 Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 241 HVDSPSOQOPLRNQVYSTNGELNVDPGTGASHNAPITAHAEVYVEAKCCFRRKRRK 300
OY 416 KTAORHK 422
DB 301 KTAORHK 307

RESULT 3
OY 09VEX2 PRELIMINARY: PRT: 422 AA.
ID 09VEX2
OY 09VEX2 01-MAY-2000 (TREMBLrel. 13, Created)
DB 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
OY 01-OCT-2001 (TREMBLrel. 18, Last annotation update)
DB CG6963 PROTEIN.
OY GISH OR CG6963.
DB Drosophila melanogaster (Fruit fly).
OY Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
DB Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OY Ephydroidea; Drosophilidae; Drosophila.
DB NCBI_TaxID=7227;
OY 11
DB SEQUENCE FROM N. A.
OY STRAIN=BERKELEY.
DB MEDLINE-20196006; PubMed-10731132;
OY Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
DB Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
OY George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
DB Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
OY Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe C.R., Pfeiffer B.D.,
DB Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
OY Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
DB Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
OY Beeson K.Y., Bens P.V., Berman B.P., Bhandari D., Bolshakov S.,
DB Borokov D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
OY Burks K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
DB Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
OY de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
DB Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
OY Durbin K.J., Evangelista C.C., Ferraz C., Ferlita S., Fleischmann W.,
DB Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
OY Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
DB Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
OY Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,
DB Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
OY Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
DB Laske P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
OY Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
DB Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
OY Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
DB Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclab J.M.,
OY Palazzolo M., Pittman G.S., Pan S., Pollard J., Puti V., Reese M.G.,
DB Releart K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
OY Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
DB Spter E., Spradling A.C., Stapleton M., Strong R., Sun E.,
OY Svitskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
DB Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
OY Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
DB Ye J., Yeh K.-P., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
OY Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
DB "The genome sequence of Drosophila melanogaster."
OY Science 287:2185-2195(2000).
DB -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
OY EMBL; AB003712; AAF5293.1; -.
DB HSP; Q06486; ICK1.
OY Flybase; FBgn0011253; gish.
DB InterPro: IPR000719; Euk_pkinase.
OY InterPro: IPR002290; Ser_thr_pkinase.
DB Pfam: PF00069; pkinase.1.
OY PROSITE; PS00107; PROTEIN_KINASE_ATP_1.
DB PROSITE; PS50011; PROTEIN_KINASE_DOM_1.

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DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Serine/threonine-protein kinase; Transferase
SQ SEQUENCE 422 AA; 48163 MW; 41DA2B7AB73DDB0F CRC64;

Query Match	Score	DB	Length
69.18;	1553;	5;	422;

[illegible]

Q9H5M4	PRELIMINARY;	PRT;	280 AA.
09H5M4			
AC	09H5M4;		
DT	01-MAR-2001 (TREMBLrel. 16, Created)		
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)		
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)		
DE	CDNA: FLJ23304 F1S, CLONE HEP13177.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
OX	NCBI_TaxId=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Kawabata A., Hikiiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,		
RA	Okhtani R., Oka T., Suuki Y., Oayashi M., Nishi T., Shibahara T.,		
RA	Tanaka T., Nakamura Y., Isogai T., Sugano S.,		
RT	"NEDO human cDNA sequencing project."		
RL	Submitted (Aug-2000) to the EMBL/Genbank/DBJ databases.		
CC	-1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.		
DR	EMBL: AK026957; BAB15601.1; -.		
DR	HSSP: 006486; 1CKI.		
DR	InterPro: IPR0000719; Euk_Pkinase.		
DR	InterPro: IPR002290; Ser_Thr_Pkinase.		
DR	Pfam: PF00069; Pkinase; 1.		
DR	SMART: SM00220; S_TKC; 1.		
DR	PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.		
DR	PROSITE: PS00108; PROTEIN_KINASE_ST; 1.		
DR	ATP-binding; Serine/threonine-protein kinase; Transferase.		
Q9	SEQUENCE 280 AA; 3265 MW; 35DELF50978039CD CRC64;		

Query Match	66.48;	Score 1492;	DB 4;	Length 280;
Best Local Similarity	99.68;	Pred. No. 6.3e-122;		
Matches 279;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;

Qy	143	MAIOLLSRMXYVNSKNLTYYDVPENPDLJROCNKKHEVHIHIDFLAEYIDPEYTKH	2020
Db	1	MAIOLLSRMXYVNSKNLTYYDVPENPDLJROCNKKHEVHIHIDFLAEYIDPEYTKH	60
Qy	203	IPYREHKSJLTGARYMSINTHLGKEOSRBDLEALGHMFYFLGSLPWOGLKADTLKER	2623
Db	61	IPYREHKSJLTGARYMSINTHLGKEOSRBDLEALGHMFYFLGSLPWOGLKADTLKER	1200
Qy	263	YOKIGDTRKRNPIALCNPPEEMATLYRYRLDFEKPXEYKTLPLFIDPEKKGYTF	3222
Db	121	YOKIGDTRKRNPIALCNPPEEMATLYRYRLDFEKPXEYKTLPLFIDPEKKGYTF	1600
Qy	323	DYADWMGRPIPTPVGSHVNDGSAATRESHTHRDRPSOOQPLRNQVSVSTNGELNVDD	3822
Db	181	DYADWMGRPIPTPVGSHVNDGSAATRESHTHRDRPSOOQPLRNQVSVSTNGELNVDD	2400
Qy	383	PTGAHSNAPITAHAEVEVEEAEKCCCFKKRKKKTAQBNK	422
Db	241	PTGAHSNAPITAHAEVEVEEAEKCCCFKKRKKKTAQBNK	280

RESULT	5			
09J076		PRELIMINARY:		PRT: 416 AA.
ID	09J076			
AC	09J076			
DT	01-OCT-2000 (TrEMBLrel. 15, Created)			
DT	01-OCT-2000 (TrEMBLrel. 15, Last sequence update)			
DT	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)			
DE	CASEIN KINASE 1 EPSILON.			
GN	CK1E.			
OS	Rattus norvegicus (Rat).			
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
CC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	NCBI_TaxID=10116;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=WISTAR;			
RA	Takano A., Shimizu K., Kani S., Bujs R.M., Okada M., Nagai K.;			
RT	"Cloning and characterization of rat casein kinase 1 e.";			
RL	Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.			
CC	-1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.			
DR	EMBL; AB042191; BAB03472.1; -			
DR	HSSP; 006486; 1CKJ.			
DR	InterPro; IPR0000719; Euk_Pkinase.			
DR	InterPro; IPR002290; Ser_Thr_Pkinase.			
DR	Pfam; PF00069; Pkinase.1.			
DR	PROSITE; PS00107; PROTEIN_KINASE_ARP; 1.			
DR	PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.			
DR	PROSITE; PS00108; PROTEIN_KINASE_ST; 1.			
DR	ATP-Binding; kinase; Serine/threonine-protein kinase; Transferase.			
SO	SEQUENCE 416 AA; 47292 MW; 38D94799A854486 CRC64;			

Query Match	42.28;	Score 948.5;	DB 11;	Length 416;
Best Local Similarity	47.68;	Pred. No. 2.7e-74;		
Matches 188;	Conservative 75;	Mismatches 107;	Indels 25;	Gaps 5

[illegible]

[illegible]

RESULT	6
09JKD0	
ID	PRELIMINARY; PRT; 416 AA.
AC	09JKD0;
DT	01-OCT-2000 (TREMBLrel. 15, Created)
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE	CASEIN KINASE I EPSILON.
OS	Mesocricetus auratus (Golden hamster).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC	Mesocricetus.
OX	NCBI_TaxID=10036;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=20237939; PubMed=10775102;
RA	Lowrey P.L., Shimomura K., Antoch M.P., Yamazaki S., Zemenides P.D.,
RA	Ralph M.R., Menaker M., Takahashi J.S.;
RT	"Positional systematic cloning and functional characterization of the
RT	mammalian circadian mutation tau.";
RL	Science 288:483-492(2000).
CC	1. SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC	EMBL: AF442336; AAF65549.1; -.
DR	HSSP: Q06486; 1CKT
DR	InterPro: IPR000719; Euk_pkinase.
DR	InterPro: IPR002290; Ser_thr_pkinase.
DR	Pfam: PF00069; pkinase; 1.
DR	PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR	PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
DR	PROSITE: PS00108; PROTEIN_KINASE_SF; 1.
KW	ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
FT	VARIANT 178 178 R -> C.
SEQUENCE	416 AA: 47308 MW: 38094799A939E86 CRC64;

	Query Match	42.2%	Score	948.5	DB11	Length	416;			
	Best Local Similarity	47.6%	Pred	2.7e-74;						
	Matches	188;	Conservative	75;	Mismatches	107;	Indels	25;	Gaps	
QY	38	LWMPNFRVGGKKTIGCGNFGEELRLGKNLYTNEYVAIKLEPIKSAPOLHLEPRFKYLGSGA	97							
Db	3	LRNGNKRRLLRGLTGSGSFGDILYGANIASOEEBAIKLECCTKHPOHLHIESKEKYKKM-DG	61							
QY	98	GEGHPGVYYGPGCGKYAAWLTELLGPSLEDLPLOCDRTFFYLKLVLMIAIDLSRMKEYHS	157							
Db	62	GVGIPSTKMGAGADYNVMWMELLGSLEDLNFCGRKPSLTKIVLLLAQMIRIETIHS	121							
QY	158	KNLIIYDVAKPENFLIGHGKNKKREHYHIIDFLAKLEYIDEPYKHHIIPYEHNLSJGTARY	217							
Db	122	KNFHRHVYKPDNKLMLGL-GKGNLYVIIDEFLAKRYRADRTQHPIPYRENKKLTSTARY	179							
QY	218	MSINTHLGKESQRDDLAEALGHMFYLFNRSLSPMOGLAKADTEKERYQIGDTKRNPPIEA	277							
Db	180	ASINETHGISQSRDDLESGLGYLWLFNUGSLPMOGUKATATKOKTERISEKKMSPIEY	239							
QY	278	LCENFPPEMAITYLRYARRLDDEFKRPDEYIRTLFTDFEKKGITTEDYDAIDVGRPLPTFY	337							
Db	240	LCKGYBEEFTSYLNFCSSLEFDKDPDYSLTRQLRNLFPHQGSSYDYVDW-----	290							

QY	338	GSVHSDSASAIITRESHTHRDRPQOQVYSSNGELVNDVPGASN-----API	392
		::: ::: ::: :::	
Db	291	---NMLKGAARNEDVDREHREHERBERMQGLGSAFTALPPEPPIGATANRLRSAAEP	347
QY	393	TAHAEEVVEEA-----KCCCFEKKKKKTKQNRK	422
		::: ::: ::: :::	
Db	348	VASTPASHRIQAGNTSPALRSADRERKVSRLR	382

RESULT	7			
099PS2		PRELIMINARY;	PRRT;	506 AA.
ID	Q99PS2			
AC	Q99PS2;			
DT	01-JUN-2001 (TrEMBLrel. 17, Created)			
DT	01-JUN-2001 (TrEMBLrel. 17, Last sequence update)			
DT	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)			
DE	CASEIN KINASE1 EPSILON-2.			
GN	CK1E-2.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	NCBI_TaxID=10116;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Takano A., Nagai K.;			
RL	Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=20359300; PubMed=10899319;			
RA	Takano A., Shimizu K., Kani S., Buys R.M., Okada M., Nagai K.;			
RT	"Cloning and characterization of rat casein kinase1."			
RL	FEBS Lett. 477:106-112(2000).			
CC	1-1 SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.			
DR	EMBL: AB056113; BAB32922.1; ..			
DR	HSP: Q06486; ICKU.			
DR	InterPro: IPR000719; Euk.pkinase.			
DR	InterPro: IPR002290; Ser_thr.pkinase.			
DR	InterPro: IPR001245; Tyr.pkinase.			
DR	Pfam: PF00069; pkinase.1.			
DR	SMART: SM00320; S.TKc.1.			
DR	SMART: SM00219; TYTKc.1.			
DR	PROSITE: PS00107; PROTEIN_KINASE_ARP.1.			
DR	PROSITE: PS50011; PROTEIN_KINASE_DOM.1.			
DR	PROSITE: PS00108; PROTEIN_KINASE_SF.1.			
KW	ATP-binding; kinase; Serine/threonine-protein kinase; Transferase.			
QC	SEQUENCE 506 AA; 56923 MW; 9DF11C50CEA96898 CRC64;			

[illegible]

Db 291 ---NMKFGAARNPEVDREHEREREEMQGLSATRALPPGPPIGATNRLSAAR 347
 QY 393 TAAAEVEVEBA-----KCCCFERRKKRTAQRHK 422
 Db 348 VASPPASRIQOAGNTSPRAISRADREKRVSWRLHR 382

RESULT 8
 Q9PU12 PRELIMINARY; PRT; 416 AA.
 AC 09PU12
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE CASEIN KINASE I EPSILON.
 GN CRE.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesodactylia; Pipridae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9445220; PubMed=10517632;
 RA Peters J.M., McKay R.M., McKay J.P., Graff J.M.;
 RT "Casein kinase I transduces wnt signals."
 RL Nature 401:345-350(1999).
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL: AF183394; AAF01032.1; -.
 DR HSP, Q06486; ICKI.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR Pfam: PF00069; pkinase.1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP.1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM.1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST.1.
 DR ATP-binding; kinase; Serine/threonine-protein kinase; Transferase.
 KW KM
 SQ SEQUENCE 416 AA; 47315 MW; F0F7CB691A4F4CDF CRC64;

Query Match 42.1%; Score 945.5; DB 13; Length 416;
 Best Local Similarity 52.2%; Pred. No. 4,8e-74;
 Matches 186; Conservative 62; Mismatches 85; Indels 23; Gaps 6;

QY 38 LAMGPNFVGGKIKGNGELRLGKNLYTNEYVAIKLEPIKSRAPOLHLEYRFYKOLGSA 97
 Db 3 LRVGKMYLGRKIGSGSGDIYLGANLATGEVAIKLECVTKHPQHIIESKFKMM-QG 61
 QY 98 GEGLPQVYTFPGCGKYNAVLELLGPSLEDFLDCDRFTFTIKTYLMTAIOQLSRREYHS 157
 Db 62 GVGIPSIKMCAGSDYNNVMVLELLGPSLEDFNFCRSKFSIKTYLLADOMISRIEYHS 121
 QY 158 KNLIVDVKPNENFLGRGNKKEHYIHIDFLAKKEYIDPETKKHIPPYREKSLTGTA 217
 Db 122 KNFHRDVKPNENFLGRL--GKGNLVIYIDFLAKKYDADTHOHIPYREKKNLIGTA 179
 QY 218 MSINTHLKEOSRRDLEALGHMFYFLRGSLLPMOGLKADTLKERYOKIGDTKRNTPIEA 277
 Db 180 ASINTHLGIEOSRRDLESLGYLMTFLGSLPMOGLKAARKQYERISSEKSTPIEV 239
 QY 278 LCENPFEMATYLRVRLDFEKPDPYLYLFTLDFEKKGYFDYAVDWGRIPIPV 337
 Db 240 LCKGVSFSTYLNFCRSLRFDDKPDYSYLRLDFENLHROGFSYDYVDM----- 290
 QY 338 GSVHVDGASA-----ITRSHTHDRPSQOQPLRNQVYSTNGELNVDPGASHN 389
 Db 291 ---NMKFGAARNPEVDREHEREREEMQGLSATRALPPGPPIGATNRLSAAR 339

RESULT 9
 Q9U8F8 PRELIMINARY; PRT; 330 AA.
 ID Q9U8F8

AC Q9U8F8;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE CASEIN KINASE I HOMOLOG 2 (CASEIN KINASE 1.2).
 GN CK1.2.
 OS Trypanosoma cruzi.
 OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
 OX NCBI_TaxID=5693;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Spadafora C., Repetto Y., Robello C., Morello A., Castanys S.,
 RA Gamarro F.;
 RT "Trypanosoma cruzi casein kinase 1 homolog 2, complete mRNA
 sequence."
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL: AF274059; AAK58696.1; -.
 DR HSP, Q06486; ICKI.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR Pfam: PF00069; pkinase.2.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP.1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM.1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST.1.
 DR ATP-binding; kinase; Serine/threonine-protein kinase; Transferase.
 KW KW
 SQ SEQUENCE 330 AA; 38093 MW; C29B3477532E72E CRC64;

Query Match 41.9%; Score 942; DB 5; Length 330;
 Best Local Similarity 53.3%; Pred. No. 7e-74;
 Matches 178; Conservative 61; Mismatches 79; Indels 16; Gaps 4;

QY 38 LAMGPNFVGGKIKGNGELRLGKNLYTNEYVAIKLEPIKSRAPOLHLEYRFYKOLGSA 97
 Db 5 LRVGKMYLGRKIGSGSGDIYLGANLATGEVAIKLECVTKHPQHIIESKFKMM-QG 64
 QY 98 G--EGLPQVYTFPGCGKYNAVLELLGPSLEDFLDCDRFTFTIKTYLMTAIOQLSRREY 155
 Db 65 GVGIPSIKMCAGSDYNNVMVLELLGPSLEDFNFCRSKFSIKTYLLADOMISRIEYHS 124
 QY 156 HSKNLIVDVKPNENFLGRGNKKEHYIHIDFLAKKEYIDPETKKHIPPYREKSLTGTA 215
 Db 125 HSKSVIHRDVKPNENFLGRL--GKGNHVIYVDFGLAKKYDRDTHOHIPYREKKNLIGTA 182
 QY 216 RYMSINTHLKEOSRRDLEALGHMFYFLRGSLLPMOGLKADTLKERYOKIGDTKRNTPI 275
 Db 183 RYCSINTHLGIEOSRRDLESLGYLMTFLGSLPMOGLKAARKQYERISSEKSTPIEV 242
 QY 276 EALCENPFEMATYLRVRLDFEKPDPYLYLFTLDFEKKGYFDYAVDWGRIPIPV 335
 Db 243 ETLCKGFAEPAEAYLYNIRSLRFEDKPDYSYLRLDFELFIREGYHVDVDM----- 296
 QY 336 PVGSHVDGASAITRSHTHDRPSQOQPLRNQ 369
 Db 297 -LKRHHEN-----LKAEGSGQEQKQDQOQRRER 324

RESULT 10
 Q9JUT5 PRELIMINARY; PRT; 367 AA.
 ID Q9JUT5
 AC Q9JUT5;
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)

DE CASRIN KINASE 1 EPSILON-3.
 GN RCKIE-3.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=WISTAR;
 RA Takano A., Shimizu K., Kani S., Buls R.M., Okada M., Nagai K.;
 RT "Cloning and characterization of rat caserin kinase 1 e.";
 RL Submitted (Apr-2000) to the EMBL/Genbank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL: AB042192; BAB03473.1; -.
 DR HSSP: 006486; 1CKJ.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR Pfam: PF00069; pkinase.1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 367 AA; 42150 MW; 546C7E2A7E41E503 CRC64;

Query Match 41.9%; Score 942; DB 11; Length 367;
 Best Local Similarity 53.3%; Pred. No. 8.2e-74;
 Matches 179; Conservative 64; Mismatches 67; Indels 26; Gaps 4;

OY 38 LMVGNFRVKKIGCGNGELALGKLVNENVAIKLEPKSRAPOLHEVRYKOLGSA 97
 DB 3 LMVGNFRVKKIGCGSGEDYLGANVSGEEVAIKLEPKSRAPOLHEVRYKMM-OG 61
 OY 98 GEGLPVYVFGCGKRYNAMVELLGLPSLEDFLDCDRTFLTKVLMIAIQLSRMEVHS 157
 DB 62 GCGIFSIRKMGAGDYNNVNMELGLPSLEDFLFCRSKRSKLTAVLLAQMSRIEYHS 121
 OY 158 KMLIYRDVKNPFLIGROGKKEHVHIIDFGLAKKEYIDETPKKHIPYREHKSLSGTARY 217
 DB 122 KNFIRHDVDPDNFLMGL-GKRGKLVYIIDFGLAKKRYDARTQHPIRENNKMLTGTARY 179
 OY 218 MSINHLGKESRRDDEALGHMFYFLRGLSPWQGLKADTLKEROKIGDKRNPPIA 277
 DB 180 ASINHLGKESRRDDEALGVLMYFNLGSLPWQGLKATKATKOKYERSEKMSPIELV 239
 OY 278 LCENPEEKATYLYRYRDLFEKPPDYELRTFLDLEFKKGYTPDYAYDWGRPIPTVY 337
 DB 240 LCKGFPSESTYLNCRSLRFDDKPDYSLRQLFRNLFRQGFSDYVYVDM----- 290
 OY 338 GSVHVDGASAITRESHHRDRPSQOQPLRNOVSS 373
 DB 291 --NMKLFQASS-----SOAQPRDNEALAS 312

RESULT 11
 O9LM62 PRELIMINARY; PRT; 442 AA.
 AC O9LM62;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE CASEIN KINASE (AT3G23340/MLM24_21).
 OS Arabidopsis thaliana (Mouse-ear cress).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 CC eucosids II; Brassicales; Brassicaceae; Arabidopsids.
 RX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=COLUMBIA;
 RA Sato S., Nakamura Y., Kaneo T., Kato T., Asamizu E., Tabata S.;
 RL Submitted (JUN-1998) to the EMBL/Genbank/DBJ databases.
 RN [2]

RP SEQUENCE FROM N.A.
 RC STRAIN=COLUMBIA;
 RX MEDLINE=20277480; PubMed=10819329;
 RA Nakamura Y.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence
 features of the regions of 4,504,864 bp covered by sixty pl and YAC
 clones.";
 RL DNA Res. 7:131-135(2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
 RA Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
 RA Ishida J., Jiang P.X., Jones T., Kamita A., Karlitz-Neumann G.,
 RA Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
 RA Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
 RA Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
 RA Yamamura Y., Yu G., Yu S., Shinzaki K., Davis R.W., Theologis A.,
 RA Ecker J.R.;
 RT "Arabidopsis cDNA clones";
 RL Submitted (Aug-2001) to the EMBL/Genbank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 DR EMBL: AB015474; BAB02278.1; -.
 DR EMBL: AY054179; AAL06840.1; -.
 DR HSSP: 006486; 1CKJ.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR Pfam: PF00069; pkinase.1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SQ SEQUENCE 442 AA; 50360 MW; A57C72ABBCB25D CRC64;

Query Match 41.9%; Score 941.5; DB 10; Length 442;
 Best Local Similarity 48.2%; Pred. No. 1.2e-73;
 Matches 184; Conservative 73; Mismatches 96; Indels 27; Gaps 7;

OY 39 MVGPNFRVKKIGCGNGELALGKLVNENVAIKLEPKSRAPOLHEVRYKOLGSA 98
 DB 4 VIGGKFLKRGKIGSGSFGELYIGINVTGEEVALKLEPKTKHPOLHESKYMLL-QGG 62
 OY 99 EGLPVYVFGCGKRYNAMVELLGLPSLEDFLDCDRTFLTKVLMIAIQLSRMEVHS 158
 DB 63 GCVPHIKMGVGNVNCMAIDLGLPSLEDFLFCRSKRSKLTAVLLAQMSRIEYHS 122
 OY 159 NLIYRDVKNPFLIGROGKKEHVHIIDFGLAKKEYIDETPKKHIPYREHKSLSGTARY 218
 DB 123 GFLHDKIRDNFLMGL-GRKANQYIIDYGLAKKRYDARTQHPIRENNKMLTGTARY 180
 OY 219 SINTHLGKESRRDDEALGHMFYFLRGLSPWQGLKADTLKEROKIGDKRNPPIA 278
 DB 181 ASINHLGKESRRDDEALGVLMYFNLGSLPWQGLKATKATKOKYERSEKMSPIELV 239
 OY 278 LCENPEEKATYLYRYRDLFEKPPDYELRTFLDLEFKKGYTPDYAYDWGRPIPTVY 337
 DB 241 CKSYSEFTSYRHYCSLRFDDKPDYSLRQLFRNLFRQGFSDYVYVDM----- 290
 OY 338 GSVHVDGASAITRESHHRDRPSQOQPLRNOVSS 373
 DB 352 IPRKHFSDASKAEVQVSEKTR 373

RESULT 12
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 AC O9FPH8;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 17, 2002, 20:21:26 ; Search time 1892.02 Seconds

(without alignments)
14035.673 Million cell updates/sec

Title: US-09-765-068-1

Perfect score: 1269
Sequence: 1 atggacatctctagtagga.....ctgtccagcgccacagtga 1269

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%

Listing first 45 summaries

Database :
1: gb_ba:*
2: gb_bhg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
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27: em_un:*
28: em_vl:*
29: em_hg_hum:*
30: em_hg_inv:*
31: em_hg_inv:*
32: em_hg_inv:*
33: em_hg_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Query Match Length DB ID Description

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2	1269	100.0	1269	6	AX250158	Sequence
3	1269	100.0	1649	9	AB042563	Homo sapi
4	1269	100.0	1968	6	AX202217	Sequence
5	1269	100.0	2066	6	BC017236	Homo sapi
6	1198	94.4	2066	6	AX239864	Sequence
7	1146.4	90.3	4417	6	AX239864	Sequence
8	1143.4	90.1	1377	6	AX239866	Sequence
9	1113	87.7	1950	6	AB042562	Homo sapi
10	979	77.1	1648	10	RN022296	Sequence
11	852.8	67.2	3552	9	AK026957	Homo sapi
12	608.8	48.0	2405	6	I73428	Sequence
13	603	47.5	1767	9	HS089896	Homo sapien
14	603	47.5	2446	9	BC020972	Homo sapi
15	577.6	45.5	1572	10	RN022297	Sequence
16	566.6	44.6	2547	10	RN022321	Sequence
17	564.8	44.5	1233	6	I73429	Sequence
18	561.8	44.3	2421	9	AF049089	Homo sapi
19	548.8	43.2	2773	9	AF049090	Homo sapi
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21	470	37.0	1162	4	BOVCKIG	Bovine case
22	299.8	23.6	1541	8	ATU48779	Arabidops
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25	293.4	23.1	2652	5	AF183394	Xenopus 1
26	292	23.0	1402	9	BC006490	Homo sapi
27	291.8	23.0	1229	10	AB042192	Rattus no
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33	291.8	23.0	1443	8	AY040071	Arabidops
34	291.8	23.0	1528	10	AB056113	Rattus no
35	291.8	23.0	1715	8	AF250343	Arabidops
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ALIGNMENTS

RESULT 1
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LOCUS AX202215 1269 bp DNA linear PAT 30-AUG-2001
DEFINITION Sequence 1 from Patent WO0153493.
ACCESSION AX202215
VERSION AX202215.1 GI:15391999
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 1269)
Donoho, G., Hibun, E., Turner, C.A., Friedlich, G., Zambrowicz, B. and
Sands, A.T.
Human Kinase protein and polynucleotides encoding the same
Patent: WO 0153493-A 1 26-JUL-2001.
JOURNAL Lexicon Genetics Incorporated (US)
FEATURES
source 1.1269
/organism="Homo sapiens"
/db_xref="taxon:9606"
LOCATION/Qualifiers

BASE COUNT 390 a 284 c 297 g 298 t
ORIGIN

Query Match 100.0%; Score 1269; DB 6; Length 1269;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1269; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 181 GGTAAAAATCTCTACACCAATGAATATGTAGCAATCAAACTGAAACCAATTAACGT 240

QY 241 gttcccaagcttcaatgaagatacagaattataaagcttgagctgagtgagtgagt 300
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RESULT 2
 AX250158 1269 bp DNA linear PAT 28-SEP-2001
 LOCUS AX250158
 DEFINITION Sequence 3 from Patent WO0166594.
 ACCESSION AX250158
 VERSION AX250158.1 GI:15864533
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 1269)
 AUTHORS Ploman, G.D., Whyte, D., Manning, G., Sudarsanam, S. and Martinez, R.
 TITLE Human protein kinases and protein kinase-like enzymes
 JOURNAL Patent: WO 0166594 A 3 13-SEP-2001;
 Sugen, Inc. (US)

FEATURES
 source
 1. 1269
 /organism="Homo sapiens"
 /db_xref="taxon:9606"

BASE COUNT 390 a 284 c 297 g 298 t
 ORIGIN

Query Match 100.0%; Score 1269; DB 6; Length 1269;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1269; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 1 ATGACACATCCTAGTAGGAAAGAAAGATGAACAAACGAACTAAACCATGGACAA 60

QY 61 aggaagtcaactgctctcgaaacatctggtctctacatcgccctctgggtcttattagt 120
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 Db 61 AGGAGTCACACCTGCTCGACCAATGCGCTCCATCGTCTCTGGGGTCTTATGAGTG 120

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 Db 181 GGTAAAAATCTCTACACCAATGAATATGTAGCAATCAAACTGAAACCAATTAACGT 240

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 Db 241 GCTCCACAGCTTCATTTAGAGTACAGATTTTATTAACAGCTTGGCAGTGAGTAAAGT 300

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Db	361	ctttggccctgagcttggaagaccttggttgacctctgtgaccgaacatttcttggaagag	420
OY	421	gttcaatgatagacatccaagctgcttctcgaatgaaatacgtgcactcaagaacctc	480
Db	421	gtgttaattatgagccatccagctgcttctcgaatgaaatacgtgcactcaagaacctc	480
OY	481	atttacccaagatgycaaagccagaagaacttcctgatattgctgcagaagcaataagaag	540
Db	481	attttaccggagatgcotaaagccagaagaacttcctgatattgctgcagaagcaataagaag	540
OY	541	catgtatatacaattatagacttggacttggcgaagaaataatattgaccccgaaaccaa	600
Db	541	catgtttatatacaattatatacatttggacttggcgaagaaataatattgaccccgaaaccaa	600
OY	601	aaacacataccttataagggaaacacaagaatttaacttgcagactgcagaatatatgtctac	660
Db	601	aaacacataccttataagggaaacacaagaatttacttgcagactgcagaatatatgtctac	660
OY	661	aacacgcactcttgcgaagaagcaaaacggagagatgatttggaaagccctaggccaatg	720
Db	661	aaacagcactcttgcgaagaagcaaaacggagagatgatttggaaagccctaggccaatag	720
OY	721	ttcagatatttcccttcggagcgacccctcccttcgcaagagactaaagctgacacattaaa	780
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OY	781	gagagatatcaaaaaatttgctgacacaaagaatacctccacttgaagctctcctgtgag	840
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OY	841	aacttccaagaggatgycgaacctcactcctcgatatgctcgaagcgagacttcttgaa	900
Db	841	aaacttccaagaggatgycgaacctcactcctcgatatgctcgaagcgagacttcttgaa	900
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OY	961	accttgacatacgtcattgattggcttggagacctatcctcactccagtaaggtcagtt	1020
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Db	1021	caagtagattctgctgacactcgcgaataactcgagaagaaccacacataagggatcgcga	1080
OY	1081	tcacaaacagcagccctctcgaataacgaatggtttagctcaacaaatggagagctgtaatt	1140
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Db	1141	gatgatgcccaagcgagcccaactcgaatcgaacaactcaagactcattgcgcgaagtggagta	1200
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AB042563	
LOCUS	AB042563 1649 bp mRNA linear PRI 23-JAN-2001
DEFINITION	Homo sapiens CSNK1G.L mRNA for casein kinase I gamma IL, complete
CDL	AB042563
ACCESSION	AB042563
VERSION	AB042563.1 GI:11177009

KEYWORDS	source	FEATURES
ORGANISM	Human sapiens cDNA to mRNA, clone_jlb:lambda ZAP human testis cDNA(Stratagene No.939201).	
REFERENCE	Homio sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. 1 (sites) Kusuda,J., Hirai,M., Tanuma,R. and Hashimoto,K. Cloning, expression analysis and chromosome mapping of human casein kinase 1 gamma (CSNK1G1): Identification of two types of cDNA encoding the kinase protein associated with heterologous carboxy-terminal sequences Cytogenet. Cell Genet. 90 (3-4), 298-302 (2000) 1124537 2 (bases 1 to 1649)	
JOURNAL	PubMed	
REFERENCE	Direct Submission Submitted (10-MAY-2000) Jun Kusuda, National Institute of Infectious Diseases, Division of Genetic Resources: 1-23-1, Toyama-cho, Shinjuku, Tokyo 162-8640, Japan (E-mail: jkusuda@nih.go.jp, URL: http://www.nih.go.jp, Tel:81-3-5285-1111(ex.2122), Fax:81-3-5285-1161) Location/Qualifiers 1. 1649 /organism="Homo sapiens" /db_xref="taxon:9606" /clone_jlb="lambda ZAP human testis cDNA(Stratagene No.939201)" /note="vector: pHCklG1-7" 113. 1381 /gene="CSNK1G1L" 113. 1381 /gene="CSNK1G1L" /codon_start=1 /product="casein kinase 1 gamma 1L" /protein_id="BAB17839.1" /db_xref="GI:11177010" /translation="MDHPSREKDERORTTPMAORSAHCSRPSGSSSSGVIAWGPNNRVYKIGCGNGELRLGKNIYNTENVVAIKLEIPSRAPOLHLEFYKQSGAGEGLI OYVTFPGCGKNNMNVLELGLSLEDLDLCDDRTTTLVTLIAIQAQLSRMEYVSKNII IRVVRKPEFLIGRQGNKEHVHIIIDFGLAKETIDEPKTHPIYREKSLTGARTK SINHLGRQESRDLDLALGLHFMWYFLRSGLPWGLADTLKERYOKIGDKNRPPIE ALCENPFEEMATYLRVVRRLDFEFKPDYELRTFDLFEKKGYFDYADWVGRIPI TPVGSVHSDGASAITRESHTHRDRPSQODLIRQVYSTNGELNVDDPTGASHNAPI TAHAEEVVEAKCCCFPFKRKKRTAQRHK"	
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RESULT 4
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LOCUS
DEFINITION Sequence 3 from Patent WO0153493.

ACCESSION AX202217
VERSION AX202217.1 GI:15392000
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS Donoho, G., Hilburn, E., Turner, C. A., Friedrich, G., Zambrowicz, B. and Sands, A. T.
TITLE Human kinase protein and polynucleotides encoding the same
JOURNAL Patent: WO 0153493-A 3 26-JUL-2001;
Lexicon Genetics Incorporated (US)
FEATURES
source
1. 1968
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BASE COUNT 539 a 482 c 473 g 474 t
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Query Match 100.0%; Score 1269; DB 6; Length 1968;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1269; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Oy	841	aacttccagagagatgycacaactcactctgatalgtltagggcgactgacttcttga	900
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DEFINITION	Homo sapiens, casein kinase 1, gamma 1, clone MGC:19461		
IMAGE:	4123494, mRNA, complete cds.		
ACCESSION	BC017236		
VERSION	BC017236.1	GI:16878051	
KEYWORDS	MGC.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
TITLE	1 (bases 1 to 2066)		
JOURNAL	Strausberg,R. Direct Submission Submitted (05-NOV-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA		
REMARK	NIH-MGC Project URL: http://mgc.ncl.nih.gov		
COMMENT	Contact: MGC help desk Email: cgabbs-remail.nih.gov Tissue Procurement: ATCC CDNA Library Preparation: Rudin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILN) DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland; Web site: http://www.nisc.nih.gov/ nisc.mgcgenhl.nih.gov Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M., Benjamin,B., Blakesley,R.W., Borkstrom,G.G., Brinkley,C., Brooks,S.,		

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RESULT 6
AX239864 4417 bp DNA linear PAT 26-SEP-2001
LOCUS AX239864 4 from Patent WO0164905.
DEFINITION AX239864
ACCESSION AX239864
VERSION AX239864.1 GI:15797470
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 4417)
AUTHORS Oland, P.J., Kapeller-Libermann, R. and Meyers, R.A.
TITLE 2504, 15977, and 14760, novel protein kinase family members and
uses thereof
Patent: WO 0164905-A 4 07-SEP-2001;
Millennium Pharmaceuticals, Inc. (US)
FEATURES
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BASE COUNT 1241 a 1006 c 1065 g 1105 t
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Best Local Similarity 91.9%; Pred. No. 0;
Matches 1268; Conservative 0; Mismatches 1; Indels 111; Gaps 1;
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DEFINITION	Sequence 6 from Patent WO0164905.		
ACCESSION	AXJ39866		
VERSION	AXJ39866.1	GI:15797472	
KEYWORDS			
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. 1 (bases 1 to 1377) Olandt,P.J., Kapeller-Jbermann,R. and Meyers,R.A. 2504, 15977, and 14760, novel protein kinase family members and uses thereof Patent: WO 0164905-A 6 07-SEP-2001; Millennium Pharmaceuticals, Inc. (US)		
JOURNAL			
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DEFINITION cds.
ACCESSION AB042562
VERSION AB042562.1 GI:11177007
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SOURCE cDNA(Stratagene, No.939201).
ORGANISM Homo sapiens
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REFERENCE 1 (sites) Hirai,M., Tanuma,R. and Hashimoto,K.
AUTHORS Kusuda,U.,
TITLE Cloning, expression analysis and chromosome mapping of human casein
JOURNAL kinase 1 gamma1 (CSNK1G1): identification of two types of cDNA
PUBMED encoding the kinase protein associated with heterologous
11124537 carboxy-terminal sequences
2 (bases 1 to 1950) cytochrome. Cell Genet. 90 (3-4), 298-302 (2000)
AUTHORS Kusuda,U.
TITLE Direct Submission
JOURNAL Submitted (10-MAY-2000) Jun Kusuda, National Institute of
Infectious Diseases, Division of Genetic Resources; 1-23-1,
Toyama-cho, Shinjuku, Tokyo 162-8640, Japan
(E-mail:jkusuda@nih.go.jp, URL:http://www.nih.go.jp,
Tel:81-3-5285-1111(ex.2122), Fax:81-3-5285-1181)
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 QY 1141 gatgatccacagc 1153
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 Db 1269 GTTAAACAACTCAG 1281
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 DEFINITION cds.
 ACCESSION U22296
 VERSION U22296.1 GI:854732
 KEYWORDS Norway rat.
 SOURCE Rattus norvegicus
 ORGANISM Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 REFERENCE 1 (Bases 1 to 1648)
 AUTHORS Zhai,L., Graves,P.R., Robinson,L.C., Italiano,M., Culbertson,M.R.,
 Rowles,J., Cobb,M.H., DePaoli-Roach,A.A. and Roach,P.J.
 TITLE Casein kinase 1 gamma subfamily. Molecular cloning, expression, and
 characterization of three mammalian isoforms and complementation of
 defects in the Saccharomyces cerevisiae YCK genes
 J. Biol. Chem. 270 (21), 12717-12724 (1995)
 JOURNAL 95279411
 MEDLINE 2 (Bases 1 to 1648)
 AUTHORS Zhai,L., Graves,P.R., Robinson,L.C., Italiano,M., Culbertson,M.R.,
 Rowles,J., Cobb,M.H., DePaoli-Roach,A.A. and Roach,P.J.
 TITLE Direct Submision
 JOURNAL Submitted (06-MAR-1995) Peter J. Roach, Biochemistry and Molecular
 Biology, University of Indiana School of Medicine, 635 Barnhill
 Drive, Indianapolis, IN 46202-5122, USA
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 ACCESSION AK026957


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IMAGE:3851613, mRNA, complete cds.
ACCESSION BC020972
VERSION BC020972.1 GI:18088089
KEYWORDS MGC.

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SOURCE human.
ORGANISM Homo sapiens
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AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 2446)
JOURNAL Direct Submission
Submitted (03-JAN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: http://mgc.ncl.nih.gov
COMMENT Contact: MGC help desk
Email: cgapds-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www.shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>
 Series: IRAC Plate: 20 Row: n Column: 18
 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 11079647.

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DEFINITION Rattus norvegicus casein kinase 1 gamma 2 isoform mRNA, complete
cds.

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VERSION U22297.1 GI:854734
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 1572)
AUTHORS Zhai,L., Graves,P.R., Robinson,L.C., Itallano,M., Culbertson,M.R.,
Rowles,J., Cobb,M.H., DePaoli-Roach,A.A. and Roach,P.J.
TITLE Casein kinase 1 gamma subfamily. Molecular cloning, expression, and
characterization of three mammalian isoforms and complementation of
defects in the Saccharomyces cerevisiae YCK genes
JOURNAL J Biol. Chem. 270 (21), 12717-12724 (1995)
MEDLINE 95279411
REFERENCE 2 (bases 1 to 1572)
AUTHORS Zhai,L., Graves,P.R., Robinson,L.C., Itallano,M., Culbertson,M.R.,
Rowles,J., Cobb,M.H., DePaoli-Roach,A.A. and Roach,P.J.
TITLE Direct Submission
JOURNAL Submitted (06-MAR-1995) Peter J. Roach, Biochemistry and Molecular
Biology, University of Indiana School of Medicine, 635 Barnhill
Drive, Indianapolis, IN 46202-5122, USA
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 DEFINITION cds
 ACCESSION U22321
 VERSION U22321.1 GI:854736
 KEYWORDS
 SOURCE Norway rat.
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 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 REFERENCE 1 (bases 1 to 2547)

AUTHORS Zhai,L., Graves,P.R., Robinson,L.C., Italiano,M., Culbertson,M.R.,
 TITLE Rowles,J., Cobb,M.H., DePaoli-Roach,A.A. and Roach,P.J.
 CASEIN KINASE I gamma subfamily. Molecular cloning, expression, and
 characterization of three mammalian isoforms and complementation of
 defects in the Saccharomyces cerevisiae YCK genes
 JOURNAL J. Biol. Chem. 270 (21), 12717-12724 (1995)
 MEDLINE 95279411
 REFERENCE 2 (bases 1 to 2547)
 AUTHORS Zhai,L., Graves,P.R., Robinson,L.C., Italiano,M., Culbertson,M.R.,
 TITLE Rowles,J., Cobb,M.H., DePaoli-Roach,A.A. and Roach,P.J.
 JOURNAL Direct Submission
 Submitted (06-MAR-1995) Peter J. Roach, Biochemistry and Molecular
 Biology, University of Indiana School of Medicine, 635 Barnhill
 Drive, Indianapolis, IN 46202-5122, USA
 location/Qualifiers
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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 17, 2002, 20:25:31 ; Search time 207.63 Seconds
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Total number of hits satisfying chosen parameters: 3472872

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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30	269.4	21.2	1014	22	AAQ06772	Polynucleotide seq
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38	262.2	20.7	2468	20	AAV71906	S. pombe CKI Hnpl
39	262.2	20.7	2469	15	AAQ70809	Protein kinase (Hh
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RESULT 1

ID AAH77991 standard; DNA; 1269 BP.

AAH77991:

13-NOV-2001 (first entry)

DE Nucleotide sequence of human protein kinase SGK248.

XX Human: protein kinase; cancer; immune disease; cardiovascular disease;

XX brain disease; neuronal disease; Alzheimer's disease; chromosome 15;

KW Parkinson's disease; multiple sclerosis; metabolic disorder;

KW peripheral nervous system disease; amyotrophic lateral sclerosis;

KW infection; ocular disease; migraine; pain; sexual dysfunction;

KW mood disorder; attention disorder; cognition disorder; hypotension;

KW hypertension; psychotic disorder; dyskinesia; transplant rejection; ss.

OS Homo sapiens.

XX

XX

XX

XX

XX

XX

PR	29-MAR-2000; 2000US-0193404.
PR	13-NOV-2000; 2000US-0247013.
XX	(SUGGE-) SUGEN INC.
PA	
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PI	Plowman GD, Whyte D, Manning G, Sudarsanam S, Martinez R;
XX	
DR	WPI: 2001-536777/59.
DR	P-PSDB; AAG67392.
PT	Nucleic acids capable of encoding human polypeptides having a kinase or
PT	kinase-like activity, useful for diagnosing a disease selected from
PT	cancers, cardiovascular disease and neuronal-associated diseases (e.g.
PT	Alzheimer's disease) -
XX	
PS	Example 1; Fig 1B; 201pp; English.
XX	
CC	The present sequence encodes a human protein kinase. The
CC	gene is located at chromosomal position 15q21.3. The kinase
CC	polypeptides are useful for diagnosing a disease or disorder
CC	selected from cancers (e.g. cancers of tissues and cancers of
CC	hematopoietic origin), immune-related diseases and disorders,
CC	cardiovascular disease, brain or neuronal-associated diseases (e.g.
CC	Alzheimer's disease, Parkinson's disease, multiple sclerosis),
CC	metabolic disorders, peripheral nervous system diseases, amyotrophic
CC	lateral sclerosis, viral infections, infections caused by prions,
CC	infections caused by bacteria, infections caused by fungi, ocular
CC	diseases, migraines, pain, sexual dysfunction, mood disorders,
CC	attention disorders, cognition disorders, hypotension, hypertension,
CC	psychotic disorders, dyskinesias, and organ transplant rejection.
CC	Kinase inhibitors are useful for treating diseases and disorders
CC	described above.
XX	
XX	
SQ	Sequence 1269 BF; 390 A; 284 C; 297 G; 298 T; 0 other;
Query Match	100.0%; Score 1269; DB 22; Length 1269;
Best Local Similarity	100.0%; Prid. No. 0;
Matches 1269; Conservative	0; Mismatches
	0; Indels
	0; Gaps
0;	
QY	1 atggaccatctctagtaggaaaggaatgaagaacaagcgacaacataaccatgacaca 60
DB	1 atggaccatctctagtaggaaaggaatgaagaacaagcgacaacataaccatgacaca 60
QY	61 agaggtgcacactgctccgcacactctgctccatcgtccctcggggtttcttagt 120
DB	61 agaggtgcacactgctccgcacactctgctccatcgtccctcggggtttcttagt 120
QY	121 ggaaccaacttcaggtgtgcgaagaagatagagtgtggaacttcggagagctcagatta 180
DB	121 ggaaccaacttcaggtgtgcgaagaagatagagtgtggaacttcggagagctcagatta 180
QY	181 ggtaaatctctcacaatgatatgtagcaatcaactggaaaccataataatcaagt 240
DB	181 ggtaaatctctcacaatgatatgtagcaatcaactggaaaccataataatcaagt 240
QY	241 gttccacagcttcattagatagattatataaacgcttggagtcgaagttaaagt 300
DB	241 gttccacagcttcattagatagattatataaacgcttggagtcgaagttaaagt 300
QY	301 ctcccaagtggtattactcttgacacatgtgggaataataatgccaatgtgtcagctc 360
DB	301 ctcccaagtggtattactcttgacacatgtgggaataataatgccaatgtgtcagctc 360
QY	361 ctggacctagcttggaggaactgtttgaacctctggccgaacatttactttgaagcg 420
DB	361 ctggacctagcttggaggaactgtttgaacctctggccgaacatttactttgaagcg 420
QY	421 gtgttaatgataagcattccagctgttcttcgaaatgataatcgtcactcaagaagctc 480
DB	421 gtgttaatgataagcattccagctgttcttcgaaatgataatcgtcactcaagaagctc 480
QY	481 attaccgaagatgtcacaagcagaagaattcctgattgtgtcacaagcagaataagaag 540

[illegible]


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FT      /*tag= a
TT      /product= "Human kinase protein"
XX
XX      WO200153493-A2.
XX      26-JUL-2001.
XX      18-JAN-2001; 2001WO-US02120.
XX      18-JAN-2000; 2000US-0176690.
XX      (LEXI-) LEXICON GENETICS INC.
XX      PA
XX      Donoho G, Hilbun E, Turner CA, Friedlich G, Zambrowicz B;
XX      PI Sands AT;
XX      WPI; 2001-442260/47.
XX      DR P-PSDB; AAU04636.
XX
XX      An isolated nucleic acid molecule encoding a novel human protein useful
XX      PT as therapeutics and to screen libraries isolate clones and prepare
XX      PT cloning and sequencing templates -
XX
XX      Claim 1; Page 31; 33pp; English.
XX
XX      The sequence represents the coding sequence of a novel human kinase
XX      CC protein. The nucleic acid sequence can be used to screen libraries,
XX      CC isolate clones and prepare cloning and sequencing templates and as
XX      CC hybridisation probes for screening libraries, and as therapeutics such
XX      CC as antisense-therapy and gene-therapy. Probes derived from the DNA
XX      CC or polypeptide sequences can be used in the identification, selection
XX      CC and validation of novel molecular targets for drug discovery.
XX
XX      Sequence 1668 BP; 539 A; 482 C; 473 G; 474 T; 0 other;

```

[illegible]

Db	530	attcacggagatgTgcAaaggccaaggaacttctctgatttgTgcAaaggccaataagaagaag	589
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Db	590	catgtttatacaatataagacttTggaactTgccaaggaatacaattgaccTcgaaaccaa	649
Qy	601	aaacacataccttataaggaacacaaaagtTtaactTggaactTgcaagatataatgtctatc	660
Db	650	aaacacataccttataaggaacacaaaagtTtaactTggaactTgcaagatataatgtctatc	709
Qy	661	aaacgcactctTgcaaaaggccaagccggaagagatattTggaagcccttaagccaatg	720
Db	710	aaacgcactctTgcaaaaggccaagccggaagagatattTggaagcccttaagccaatg	769
Qy	721	tctatgtatttctctTgcAaaggccaactccctctTgcaaaagactcaagctTgacacatataa	780
Db	770	tctatgtatttctctTgcAaaggccaactccctctTgcaaaagactcaagctTgacacatataa	829
Qy	781	gagagatatcaaaaatTggtTgacacccaagaagaatactccaatTggaagctTctcgttag	840
Db	830	gagagatatcaaaaatTggtTgacacccaagaagaatactccaatTggaagctTctcgttag	889
Qy	841	aacttccagaaggagatTggaacactcactcgttatTgtaaggcgaactTgactctTgtaa	900
Db	890	aacttccagaaggagatTggaacactcactcgttatTgtaaggcgaactTgactctTgtaa	949
Qy	901	aaactcgtatTgataTttacTggaacccctctTcacagacactctTtTgaaaagaagaagctac	960
Db	950	aaactcgtatTgataTttacTggaacccctctTcacagacactctTtTgaaaagaagaagctac	1009
Qy	961	aacttTgacataTgctatTgattTggtTgTggaagactatactcactcactcagtagTgcagt	1020
Db	1010	aacttTgacataTgctatTgattTggtTgTggaagactatactcactcactcagtagTgcagt	1069
Qy	1021	cagctagattctTgTgatactTgcaataaactcgcgaagaagccacacatataggatcgcga	1080
Db	1070	cagctagattctTgTgatactTgcaataaactcgcgaagaagccacacatataggatcgcga	1129
Qy	1081	tcacaacagcagccctctTgcAaactcagTtgTttagctTcaacaatTgagagctTgatatgt	1140
Db	1130	tcacaacagcagccctctTgcAaactcagTtgTttagctTcaacaatTgagagctTgatatgt	1189
Qy	1141	gatgatcccaTggaaggccaactccaatTgcaacaatcacaagctcatTgTcgagTtgagTta	1200
Db	1190	gatgatcccaTggaaggccaactccaatTgcaacaatcacaagctcatTgTcgagTtgagTta	1249
Qy	1201	gtggaagaagaagctaaTgctcTgctTtctcttaagaaggaagaagaagaagctTgctaagc	1260
Db	1250	gtggaagaagaagctaaTgctcTgctTtctcttaagaaggaagaagaagaagctTgctaagc	1309
Qy	1261	cacaagtTga 1269	
Db	1310	cacaagtTga 1318	
RESULT 3			
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ID	AAS08536 standard; cDNA; 1968 bp.		
XX	AAS08536:		
XX	26-SEP-2001 (first entry)		
XX	DNA encoding human kinase-like protein.		
XX	Human; kinase protein; hybridisation probe; therapeutic; gene therapy::		
KM	antisense-therapy; drug screening; ss.		
XX	Homo sapiens.		
XX	WO200153493-A2.		
XX			

XX	Key	Location/Qualifiers
FH	CDS	370..1638
FT		/*tag -a
FT		/product= "Human PKIN-10 protein"
XX		
PN	WO200196547-A2.	
XX		
PD	20-DEC-2001.	
XX		
PF	14-JUN-2001; 2001WO-US19444.	
XX		
PR	15-JUN-2000; 2000US-212073P.	
PR	23-JUN-2000; 2000US-213467P.	
PR	30-JUN-2000; 2000US-215651P.	
PR	07-JUL-2000; 2000US-216605P.	
PR	13-JUL-2000; 2000US-218372P.	
PR	25-AUG-2000; 2000US-228056P.	
XX		
PA	(INCY-) INCYTE GENOMICS INC.	
PI	Yue H, Lal P, Bandman O, Borowsky ML, Au-Young J, Lu Y;	
PI	Gandhi AR, Tribouley CM, Walla NK, Yao MG, Lu DM, Greenwald SR;	
PI	Ramkumar J, Griffin JA, Kearney L, Buford N, Nguyen DB, Tang YT,	
PI	Baughn MR, He A, Thornton M, Hafalia A, Patterson C, Gururajan R;	
P1	Lo TP, Khan F, Recipon SA, Azimzal Y, Policky JL, Ding L;	
PI	Grether M, Elliott VS, Thangaveilu K, Batra S, Ison CH;	
XX		
DR	WPI: 2002-090207/12.	
DR	P-Psdb; AAEL6266.	
XX		
PT	New polypeptides, useful for diagnosing, treating or preventing	
PT	diseases of growth and development, cardiovascular and lipid, and	
PT	diseases such as cancer, comprise human kinase polypeptides	-
PS	Claim 5; Page 183; 197bp; English.	
XX		
CC	The invention relates to human kinase PKIN proteins and their	
CC	corresponding cDNAs. A composition containing PKIN agonist is useful for	
CC	treating a disease or condition associated with decreased expression of	
CC	PKIN and a composition comprising PKIN antagonist is useful for treating	
CC	a disease or condition associated with overexpression of PKIN. The	
CC	disorders include cancer (leukemia, adenocarcinoma, lymphoma, melanoma,	
CC	myeloma, sarcoma, teratocarcinoma, Hodgkin's disease), immune disorder	
CC	(Acquired Immune Deficiency Syndrome (AIDS)), asthma, Addison's disease,	
CC	atherosclerosis, anaemia, allergies, adult respiratory distress syndrome,	
CC	autoimmune thyroiditis, gout, bronchitis, Crohn's disease, diabetes	
CC	mellitus, multiple sclerosis, good pasture's syndrome, Graves' disease,	
CC	osteoarthritis, osteoporosis, pancreatitis, psoriasis, Reiter's syndrome,	
CC	rheumatoid arthritis, Sjogren's syndrome, warts, ulcerative colitis,	
CC	bacterial, parasitic, fungal, viral, protozoal and helminthic infections)	
CC	growth and development disorders (arteriosclerosis, cirrhosis, hepatitis,	
CC	Cushing's syndrome, hypothyroidism, cerebral palsy, cataracts), cardio	
CC	vascular disease (arteriovenous fistula, hypertension, vasculitis,	
CC	aneurysms, congestive heart failure, angina pectoris, myocarditis,	
CC	ischemic heart disease, chronic bronchitis, lung tumours); lipid	
CC	disorder (fatty liver, Fabry's disease, Niemann-Pick's disease,	
CC	hypercholesterolaemia, obesity). PKIN DNA is useful for assessing	
CC	toxicity of a test compound and in gene therapy. The present sequence	
CC	is human PKIN-10 cDNA.	
XX		
SQ	Sequence 1689 BP; 495 A; 391 C; 399 G; 404 T; 0 other;	
Query Match	99.9%; Score 1267.4; DB 24; Length 1689;	
Best Local Similarity	99.9%; Pied. No. 0;	
Matches 1268; Conservative	0; Mismatches 1; Indels 0; Gaps	0
Oy	1 atggaccatcctctgtaggaagaagatgaagaacgcggacaactaaacctggcacaa 60	
Dbb	370 atggaccatcctctgtaggaagaagatgaagaacgcggacaactaaacctggcacaa 429	
Oy	61 agaggtcacactgtctcgaccatctggtctccatactgctcttggttttatggtg 120	

Db	430	aggggtgcacactgctcttcgcaccatctggctctctactgtctctctggggttcttatgtg	489
Qy	121	ggaccaccaactctcaaggtcttgcgaagaatagatgtggaagacttcggaagctcagatta	180
Db	490	ggaccaccaacttcaggtgttgcgaagaatagatgtgtgggaacttcggaagctcagatta	549
Qy	181	ggttaaaatctctcaccacaatgaatatgtatgcataccaactcgaaccataaaatccagt	240
Db	550	ggttaaaatctctcaccacaatgaatatgtatgcataccaactcgaaccataaaatccagt	609
Qy	241	gtccacagctctcatatagatgaacagatttaaaacagcttcgcagtcagtcgaagt	300
Db	610	gtccacagctctcatatagatgaacagatttaaaacagcttcgcagtcagtcgaagt	669
Qy	301	ctccacagcgtgtatctactttgcaccatgtgtggaaaataatgcatalggtgtcttgagctc	360
Db	670	ctccacagcgtgtatctactttgcaccatgtgtggaaaataatgcatalggtgtcttgagctc	729
Qy	361	cttggcccttagcttgcggagacgtgtttgacacctgtgcaccgaacattactttgaagcg	420
Db	730	cttggcccttagcttgcggagacgtgtttgacacctgtgcaccgaacattactttgaagcg	789
Qy	421	gtgttaatagatgcacaccagctgcgtcttcgcgaatggaatcgtgcaccgaagaacctc	480
Db	790	gtgttaatagatgcacaccagctgcgtcttcgcgaatggaatcgtgcaccgaagaacctc	849
Qy	481	atttacccgagatgtccaaagccagaagaacttcctctatgtgtcgaataagcatalgaagaag	540
Db	850	atttacccgagatgtccaaagccagaagaacttcctctatgtgtcgaataagcatalgaagaag	909
Qy	541	catgtatacacatataagactcttgacatgctgcaccgaagaatacatgtgaccccgaaaccaa	600
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Qy	601	aaacaacatccttctatggagacaacaaaagtcttacccggagactcgaagatatgtctctc	660
Db	970	aaacaacatccttctatggagacaacaaaagtcttacccggagactcgaagatatgtctctc	1029
Qy	661	aaacgcacactcttgcgaagaagcgaagaagccggagagatgtatgtgaagcccttaagccatalg	720
Db	1030	aaacgcacactcttgcgaagaagcgaagaagccggagagatgtatgtgaagcccttaagccatalg	1089
Qy	721	ttcatgtattctcttcgcgaagcagctccctccctgcgcaagactccaagctcgaacatlaaa	780
Db	1090	ttcatgtattctcttcgcgaagcagctccctccctgcgcaagactccaagctcgaacatlaaa	1149
Qy	781	gagagatatcaaaaatgtgtgcacccaagaagaataatcccatgtgaagctcttcgtgag	840
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Qy	841	aacttccagggagatgaggaacaactaccttcgatatgtcagcggagactgcactcttgaa	900
Db	1210	aacttccagggagatgaggaacaactaccttcgatatgtcagcggagactgcactcttgaa	1269
Qy	901	aaacctgattatggaatttaacggaacctcttcacagacctcttgaagaagaagctac	960
Db	1270	aaacctgattatggaatttaacggaacctctctcacaagacctcttgaagaagaagctac	1329
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Qy	1021	cacgtagattcttgcatactgcgaataaacccggaagaagccacacacataagggatccggca	1080
Db	1390	cacgtagattcttgcatactgcgaataaacccggaagaagccacacacataagggatccggca	1449
Qy	1081	tcacaacagcagcctctcttcgaaaaatcaggtgtgttagcttcaacaatgtgaagcttgatgt	1140
Db	1450	tcacaacagcagcctctcttcgaaaaatcaggtgtgttagcttcaacaatgtgaagcttgatgt	1509
Qy	1141	gatgatccacaggagcccaactccaatgcacaaatcaagcttcacgtgcgaggttgaggtat	1200

Query	Subject	Accession	Length	Score	E-value	Identity	Mismatches	Indels	Gaps
Qy	1201	g1ggaaggaagctaagtcgtctgttcttcaagaaggaagaaagactgtccagcgc	1260	95.7%	1.21e-8	DB 22	Length 1754;		
Db	1570	gtcgaaggaagctaagtcgtctgttcttcaagaaggaagaaagactgtccagcgc	1629	99.8%	0.0				
Qy	1261	cacaagtga 1269							
Db	1630	cacaagtga 1638							
RESULT 5									
ID	AAH21501	standard; CDNA; 1754 BP.							
XX	AAH21501;								
AC	AAH21501;								
DT	10-AUG-2001	(first entry)							
XX									
DE	Human casein kinase 48 encoding cDNA SEQ ID NO:1.								
XX									
KW	Human; casein kinase 48; cytosolic; immunomodulatory; antiinflammatory;								
KW	virucide; gene therapy; diagnosis; treatment; malignant tumour;								
KW	haemopathy; HIV infection; immunological disease; inflammation; ss.								
OS	Homo sapiens.								
FT	Key	Location/Qualifiers							
FT	CD5	199..1515							
FT		/tag= a							
FT		/product= "casein kinase 48"							
PN	MO200129228-A1.								
XX									
PD	26-APR-2001.								
XX									
PE	16-OCT-2000; 2000MO-CN00330.								
XX									
PR	18-OCT-1999; 99CN-0116987.								
XX									
PA	(SHAN-) SHANGHAI BIO ROAD GENE DEV LTD.								
XX									
PI	Mao Y, Xie Y;								
XX									
DR	WPI: 2001-282163/29.								
DR	P-PSDB: AAB97904.								
XX									
PT	Human casein kinase 48 and encoded polynucleotide, applicable in								
PT	diagnosis and treatment of malignant tumor, hemopathy, HIV infection,								
PT	immunological diseases and various inflammation								
XX									
PS	Claim 6; Page 22-23; 30pp; Chinese.								
XX									
CC	The present sequence encodes human casein kinase 48 (CK48). CK48 has								
CC	cytosolic, immunomodulatory, antiinflammatory and virucide activity,								
CC	and can be used in gene therapy. The CK48 protein and polynucleotide								
CC	sequences can be used in the diagnosis and treatment of malignant								
CC	tumour, hemopathy, HIV infection, immunological diseases and various								
CC	inflammation.								
XX									
SQ	Sequence 1754 BP; 536 A; 372 C; 389 G; 457 T; 0 other;								
Query Match									
Best Local Similarity	95.7%	Score 1213.8;	DB 22;	Length 1754;					
Matches 1215; Conservative	0;	Mismatches	2;	Indels	0;	Gaps	0;		
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Db	199	atggacatccctcagtaggaaaggaatgaaacaaacgacacactaaacactatgacaa	258						
Qy	61	aggagtagcacactgctctcagaccatctgctctcattcgtctctctgggtcttattgtg	120						

Dh	259	agagagtgcaacatgctctccgaacatctgctccctccatccgctccctctgtggttctttagt	318
Qy	121	ggaccacaacttcagaaggtttcgcagaagagataagatgtctggaaacttcggaagctccagatta	180
Dh	319	ggaccacaacttcagaaggtttcgcagaagagtagatgtctggaaacttcggaagctccagatta	378
Qy	181	ggtaaaaatctctacaccaatgataatgtagaaatcaaacttgaaaccaataaaatcaagt	240
Dh	379	ggtaaaaatctctacaccaatgataatgtagaaatcaaacttgaaaccaataaaatcaagt	438
Qy	241	gctccacagcttcaattttagtaacagattttataaacaagctctggcagtgtaagtgaggt	300
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Qy	481	atttcacgaagtgtcaaacgacagagaactctccctgtctgtctgcacagaagcaataagaagag	540
Dh	679	atttcacgaagtgtcaaacgacagagaactctccctgtctgtctgcacagaagcaataagaagag	738
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Dh	739	catgttatcacatbatagactctgtgcctctggccgaaggaatatactgaccccggaacaaa	798
Qy	601	aaacacataacttatagggaaacaaaagaatttaactctggaactcgaagataatagtctacc	660
Dh	799	aaacacataacttatagggaaacaaaagaatttaactctggaactcgaagataatagtctacc	858
Qy	661	aaacagacatcttggcaaaagacaaagccggagagaatttggaaagcccttaagccatactg	720
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Dh	1039	aaacttccagagggatgggcaaaccttaacttcggtatgtctcagggagacttgatattctcttga	1091
Qy	901	aaactgttatctggaatttaacggaacctcttcaacaagacctcttgaagaagaagctac	960
Dh	1099	aaactgttatctggaatttaacggaacctcttcaacaagacctcttgaagaagaagctac	1151
Qy	961	aaacttgcatactgcctatgattggtgtggagaacctatctctacatccagtaagtgtaagt	1021
Dh	1159	aaacttgcatactgcctatgattggtgtggagaacctatctctacatccagtaagtgtaagt	1211
Qy	1021	caagtagattcttggtgatattctgcgaataatctcggagaagcgacacacataatgaggttcggca	1081
Dh	1219	caagtagattcttggtgatattctgcgaataatctcggagaagcgacacacataatgaggttcggca	1271
Qy	1081	tcacaacagcagctctctcgaaatcagatgtgttagcttcaacaaatgagagctgtgaagt	1140
Dh	1279	tcacaacagcagctctctcgaaatcagatgtgttagcttcaacaaatgagagctgtgaagt	1331
Qy	1141	gatgatccacaggagaccacatcccaatgtgcacaaatcaacagctcatgctcggaagtgtagta	1201
Dh	1339	gatgatccacaggagaccacatcccaatgtgcacaaatcaacagctcatgctcggaagtgtagta	1391

QY 1201 gtgaggaagtaagt 1217
1399 gtgaggaagtaagt 1415

RESULT 6

AAH78262 standard; cDNA; 4417 BP.

AAH78262;

26-NOV-2001 (first entry)

Nucleotide sequence of human kinase 15977.

Human; kinase; 2504; 15977; 14760; cellular proliferative disorder;
cellular differentiative disorder; neural disorder; immune disorder;
cardiovascular disorder; liver disorder; skin disorder;
skeletal muscle disorder; bone metabolism; cardiovascular disorder;
viral disease; pain; metabolic disorder; blood vessel disorder;
hepatic disorder; liver disorder; ss.

OS Homo sapiens.

Key Location/Qualifiers

FT CDS 337..1716

FT /tag- a

FT /product- "Kinase"

PN W0200164905-A2.

PD 07-SEP-2001.

PE 28-FEB-2001; 2001MO-US06525.

PR 29-FEB-2000; 2000US-0186061.

PA (MILL-) MILLENNIUM PHARM INC.

PI Olandt RJ, Kapeller-Libermann R, Meyers RA;

DR WPI; 2001-570697/64.

DR P-PSDB; AAG67542.

XX New protein kinase family polypeptides for treating hematopoietic

PT neoplastic disorders, immune disorders, cardiovascular disorders and

PT disorders of blood vessels

PS Claim 2; Fig 4A-C; 145pp; English.

XX The present sequence encodes human kinase 15977. The specification

CC also describes kinases 2504 and 14760. The kinase polypeptides and

CC polynucleotides are used to treat cellular proliferative or

CC differentiative disorders, neural disorders, immune disorders,

CC cardiovascular disorders, liver disorders, skin disorders and skeletal

CC muscle disorders. They may also be used for controlling disorders

CC associated with bone metabolism, cardiovascular disorders, viral

CC diseases, pain or metabolic disorders, blood vessel

CC disorders, and hepatic or liver disorders.

XX Sequence 4417 BP; 1240 A; 1006 C; 1066 G; 1105 T; 0 other;

Query Match 90.2%; Score 1144.8; DB 22; Length 4417;

Best Local Similarity 91.8%; Pred. No. 0;

Matches 1267; Conservative 0; Mismatches 2; Indels 111; Gaps 1;

QY 1 atggacatctctagtaggaagaagatgaaagacacgacgaacataaccatgacaa 60

Db 337 atggacatctctagtaggaagaagatgaaagacacgacgaacataaccatgacaa 396

QY 61 agagatgacacgtctctgcacacatctgctctccatcgtctctggtttctatggtg 120

Db 397 agagatgacacgtctctgcacacatctgctctccatcgtctctggtttctatggtg 456

QY 121 gaaccaactctcagggttgcgaagaagatagatgtggaacttcgagagccagatta 180

Db 457 gaaccaactctcagggttgcgaagaagatagatgtggaacttcgagagccagatta 516

QY 181 ggtaaaaatctcaccacaaatgatatgtatgacaaacttgaccacaaataatcagt 240

Db 517 ggtaaaaatctcaccacaaatgatatgtatgacaaacttgaccacaaataatcagt 576

QY 241 gctccacagcttcatatagatgacagatttataaagcttggcagttgagtgaaagt 300

Db 577 gctccacagcttcatatagatgacagatttataaagcttggcagttgagtgaaagt 636

QY 301 ctcccaaggtgtactaactcttgacacatgtggaataataatgcattggtgagctc 360

Db 637 ctcccaaggtgtactaactcttgacacatgtggaataataatgcattggtgagctc 696

QY 361 ctggccctagcttgagagctgttgacactctgtgacgaacattacttgaagag 420

Db 697 ctggccctagcttgagagctgttgacactctgtgacgaacattacttgaagag 756

QY 421 gtgttaatgatacgaatccagctgcttctcgaatggaatacgtgacactcaagaacctc 480

Db 757 gtgttaatgatacgaatccagctgcttctcgaatggaatacgtgacactcaagaacctc 816

QY 481 attaccgagatgtcaagccagagaactctcgtatgtgtgcacaaagcaataagaag 540

Db 817 attaccgagatgtcaagccagagaactctcgtatgtgtgcacaaagcaataagaag 876

QY 541 catgtatacacattatagactttgagctgccaaggaatacatgtgcccgaacaaa 600

Db 877 catgtatacacattatagactttgagctgccaaggaatacatgtgcccgaacaaa 936

QY 601 aaacacataccttataaggaacacaaagttaacttgaactgcgaataatgtctatc 660

Db 937 aaacacataccttataaggaacacaaagttaacttgaactgcgaataatgtctatc 996

QY 661 aacacgacatctggaacaaagcgaagagatgatttgaagccctagaccatag 720

Db 997 aacacgacatctggaacaaagcgaagagatgatttgaagccctagaccatag 1056

QY 721 ttcatgtatttctctcgaagcagctccctcgtgaagagactcaaggttgacattaaa 780

Db 1057 ttcatgtatttctctcgaagcagctccctcgtgaagagactcaaggttgacattaaa 1116

QY 781 gagagatatcaaaaattgttgacacaaagagatctccattgaaagctctgtgag 840

Db 1117 gagagatatcaaaaattgttgacacaaagagatctccattgaaagctctgtgag 1176

QY 841 aacttccagagagatggaacactctcogatatgtcagggagacttgacttttga 900

Db 1177 aacttccagagagatggaacactctcogatatgtcagggagacttgacttttga 1236

QY 901 aaactgtattatgattttagagacaccttccacaaactcttggaaagaaggttac 960

Db 1237 aaactgtattatgattttagagacaccttccacaaactcttggaaagaaggttac 1296

QY 961 accttgaatcgcctatgattgtgttgagagacatttccactcagttgagtgagtt 1020

Db 1297 accttgaatcgcctatgattgtgttgagagacatttccactcagttgagtgagtt 1356

QY 1021 cactgtagatctgtgtcatctgcaataactcogagaagccacacataagagtcgcca 1080

Db 1357 cactgtagatctgtgtcatctgcaataactcogagaagccacacataagagtcgcca 1416

QY 1081 tcacaaagcagcctcttgcgaat----- 1104

Db 1417 tcacaaagcagcctcttgcgaatlcagaatgtatcatcagaagcgcgagagagtgagaa 1476

QY 1105 ----- 1104

Db 1477 attcagccagcgcgcagcaatactatacctaactgctcactgctgcagaccgc 1536
 Qy 1105 -----caagtgttagctcaaccaatgagagctgaattgatcc 1149
 |||||||
 Db 1537 catggggatcatgacgaggtgttagctcaaccaatgagagctgaattgatcc 1596
 Qy 1150 acggagaccacatccaatgacacatcaacagctcagcaggtgagtagtgagaa 1209
 |||||||
 Db 1597 acggagaccacatccaatgacacatcaacagctcagcaggtgagtagtgagaa 1656
 Qy 1210 gctaaagctcgtcttctttaaagagaagaagagactgctcagcgcacaaatga 1269
 |||||||
 Db 1557 gctaaagctcgtcttctttaaagagaagaagagactgctcagcgcacaaatga 1716
 |||||||

RESULT 7
 ID AA070827 standard; cDNA; 2405 BP.
 AC AA070827;
 DT 17-MAR-1995 (first entry)
 DE Protein kinase (CKIgamma1Hu) coding sequence.
 XX
 KM Protein kinase; immunogen; antibody; protein-tyrosine kinase;
 KM protein-serine/threonine kinase; recombination; repair; screening;
 KM detection; casein kinase; ss.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 67..1200
 FT /*tag= a
 FT /product= Protein kinase.
 FT
 XX W09417189-A.
 PD 04-AUG-1994.
 XX
 PF 21-JAN-1994; 94WO-US00795.
 XX
 PR 21-JAN-1993; 93US-0008001.
 XX
 PA (SALK) SALK INST BIOLOGICAL STUDIES.
 XX
 PI Hoekstra MF;
 XX
 DR WPI: 1994-264102/32.
 DR P-PSDB; AAR56529.
 XX
 PT Wild-type and mutant protein kinase genes and encoded
 PT polypeptide(s) - Useful in screening for compositions which may
 PT effect DNA double strand break repair activity
 XX
 PS Claim 10: Page 97-99; 121pp; English.
 XX
 CC This sequence encodes a protein kinase which is an HRR25-like
 CC protein. Host cells stably transformed with the protein kinase
 CC encoding DNA may be used for the expression of the protein kinase
 CC such that the expressed protein is "displayed" on the host cell
 CC surface. The cells may then be used as immunogen for the production
 CC of antibodies. The host cells may also be used for the large scale
 CC production of the protein kinase; the expressed protein being either
 CC isolated from the cell surface or from the culture medium.
 CC Recombinant HRR25 like proteins display a number of properties which
 CC are unique among the eukaryotic protein kinases e.g. the HRR25
 CC protein possesses both protein-tyrosine kinase and
 CC protein-serine/threonine kinase activities. Also, HRR25 operates to
 CC promote repair of DNA strand breaks at a specific nucleotide sequence
 CC and is the only protein kinase known to have such
 CC recombination/repair promoting activity. Recombinant HRR25-like
 CC proteins and host cells expressing them are useful in screening

CC methods designed to examine the effects of various compositions on
 CC DNA break repair and protein kinase activities of the protein. The
 CC HRR25-like proteins are casein kinase class I protein kinases.
 CC
 XX
 SO Sequence 2405 BP; 849 A; 392 C; 486 G; 678 T; 0 other;

Query Match 48.0%; Score 608.8; DB 15; Length 2405;
 Best Local Similarity 71.2%; Pred. No. 1.3e-180;
 Matches 880; Conservative 0; Mismatches 337; Indels 19; Gaps 5;

Qy 1 atggacatcctagtaggaaaggatgaaagacaaagacacaaacccaatgacaa 60
 |||||
 Db 25 atggaataataaagaagaagaacaaagacaaatcagatgataatgacgcagctagtg 84
 Qy 61 aggaagtcacacgtctctgcacccctcgtccctcctcgtctcttgggtttatggtg 120
 |||||
 Db 85 cgatcgagacacacacactcggagacacttgggtcttcacg--tctgagtttaatggt 141
 Qy 121 ggaacacatcagaggttgcaagaagataagatgtggaactcggagagctcagatta 180
 |||||
 Db 142 ggaactacttaagatgttgaaaaaaatgtgatgtgcaatttggaagaattcagatta 201
 Qy 181 ggtaaaaatctctacacaaatgaaatgtagcaaatcaactggaacaaataaatacagt 240
 |||||
 Db 202 gggaaaaattatcacaaatgaaatgtatgtgcaattagtgagccatgaaatcaaga 261
 Qy 241 gctccagagcttcttagatagtagatattatataaagcttgcaatgacagtgagagt 300
 |||||
 Db 262 gcaccacagctacatttggaaatagatattcataagatgaa--gatctggagatggt 318
 Qy 301 ctccacagtggtatactatttgacacatgttggaataataatgacatggtgtgagctc 360
 |||||
 Db 319 ataccctaaagttaactatttgcgcctctgtgtaataaacaatgctatggtgtgagctg 378
 Qy 361 ctggtccctagcttgaggagactgttgcacctctgtgacagcaattacttgaagagc 420
 |||||
 Db 379 ctggacactagtttggaagactgttgcactgtgtgacagaacatttctcttaaaaaa 438
 Qy 421 ggttaagttagtcacatcgtcttctcgaatggaaatcgtgacactaaagaacactc 480
 |||||
 Db 439 gttctatgataagctacacactgattctctgcagtgaaatgctcactcaaaagacttg 498
 Qy 481 attaccagatgacaaagcagaaactcctgattgtgcagacaaagcaataaagaagag 540
 |||||
 Db 499 atatacagagatgaaacactcgaactcttcttaataagacagcagaaacaaacccag 558
 Qy 541 catgtataacattatagacttggactggcagaagaatactgacccgaaaccaa 600
 |||||
 Db 559 caagttatcacattatagatttgggttgcaagaagataatattgctcggagacaag 618
 Qy 601 aaacactactcttaaggaacacaaagaatttaactgtgaactgaaagatatgtcattc 660
 |||||
 Db 619 aaacacatcacattacagaaacaaagacacttaacgaagacagtagataatgagata 678
 Qy 661 aacacagactctgcaaaagcagaagcggagagatattgtgaagccctagggccatag 720
 |||||
 Db 679 aacacacatttaggaaaaaagacaagaagtagaagacgatttagaggtttagtgcatag 738
 Qy 721 ttcattatctctcgaagcagcctccctgtggaagacaaagctgacacattaaa 780
 |||||
 Db 739 ttcattatctctcgaagcagcctccctgtggaagacaaagctgacacattaaa 798
 Qy 781 gagagataataaaatgtgtgacacaaagaagaatctccattgaagctctctgag 840
 |||||
 Db 799 gagaggtatagaataattgtgagatacaaaacgggtctacacacaaagagtgattagaa 858
 Qy 841 aacttccagaaggagatggaacactcctcagatgtgcagagcagctctcttgaa 900
 |||||
 Db 859 aatttccagaagaagaatggaacactatctcgttaigttaagaagcagcttttttgaa 918
 Qy 901 aaactgtattatagatttaacgacccctctcagacactctttgaaagaagctac 960
 |||||

OY	973	gcctatgattgggttgggaacctatttcctactccagttgggtcagttacgttaattct	1032
Db	835	gaattactgcttgatttggtaaaccagtctgcctactccagttgggtcagttacgaagaatct	894
OY	1033	ggtgatcttgataaactcgagaagccacaacacataggagatcggccatccaacaagcacg	1092
Db	895	gctctgtcatcaaca---gagaagcacacaaccaagaagataagatgcataacatccaa-	950
OY	1093	cctctcgaaatcagctggtttagctcaaccaatgtgagagctgaatttgtatgccacg	1152
Db	951	-----aacccggttctgaagttctctacaatatggagagttaaacccagatgaccccac	1002
OY	1153	ggagccaccticcaatgacccaatcacagctcatgctcaggttggaggtagtgaggaagct	1212
Db	1003	gcag-acgttcaaatgacccaatccacagccccctactgaagtagaagtgatgtgaac	1061
OY	1213	aagtgctgctgttctcttaagag	1236
Db	1062	aactgcagaaaagctgtgaacatg	1085
RESULT 10			
AAQ92963			
ID	AAQ92963	standard; cDNA; 1233 BP.	
XX	AAQ92963;		
AC			
XX			
DT	25-JAN-1996	(first entry)	
DE	Human HRR25-like casein-kinase-I CKI-gamma-2Hu gene.		
XX			
KW	Casein-kinase-I; HRR25; protein-tyrosine-kinase; CKI-gamma-2Hu;		
KM	protein-serine/threonine-kinase; enzyme; DNA repair;		
KW	DNA recombination; ss.		
OS	Homo sapiens.		
XX			
FH	Key	Location/Qualifiers	
FT	CDS	1..1041	
FT		/*tag-a	
XX			
PN	W09519993-A1.		
PD			
XX	27-JUL-1995.		
PE			
XX	23-JAN-1995; 95MO-USO0955.		
PR			
XX	21-JAN-1994; 94US-O185359.		
PA			
XX	(SALK) SALK INST BIOLOGICAL STUDIES.		
P1	Hoekstra MF;		
XX			
DR	WP1: 1995-269419/35.		
XX	P-PsDB; AAR/6626.		
PT			
PT	New monoclonal antibodies against human casein Kinase class I		
PT	enzymes - useful for pulficc. and determ. of these enzymes and to		
PT	modulate their receptor-ligand binding, also new hybridomas		
XX			
PS			
XX	Disclosure; Page 104; 125pp; English.		
CC	This human casein-kinase-I (CKI-gamma-2Hu) gene which is a homolog		
CC	of a DNA recombination and repair gene called HRR25 (HO and/or		
CC	radiation repair) possesses both protein-tyrosine-kinase and protein		
CC	serine/tyrosine-kinase activities. HRR25 operates to promote repair		
CC	only DNA strand breaks at a specific nucleotide sequence and is the		
CC	only protein-kinase known to have such recombination/repair		
CC	promoting activity. DNA encoding HRR25 can be used to isolate and		
CC	identify related sequences, while recombinant HRR25, or cells		
CC	expressing it, can be used to screen compounds for their effects		
CC	on DNA repair and kinase activities.		
XX			

Seq	Sequence	1233 BP;	432 A;	214 C	260 G;	327 T;	0 other:
Query Match	44.5%;	Score	564.8;	DB	16;	Length	1233;
Best Local Similarity	72.7%;	Pred. No.	6,1e-167;				
Matches	803;	Conservative	0;	Mismatches	282;	Indels	19;
						Gaps	
QY	133	agggttgcgaagaatagatagatctgaggacttcctggagagctcaagattggtataaatctc	192				
Db	1	aggattgcaaaaaaaattggaatgctggaattcttggaatcagattcagtggaataattca	60				
QY	193	tacccaatgatatgttgggaatccaacttggaaccataataatcagctgctccacaagctt	252				
Db	61	tacacaatgaaatctgaggcaatlaagcttggagcccaatgaataacagacaccacaagcta	120				
QY	253	cattatgagtaacaatttataaaccagcttgcagctgcagctgcagctgcagctgcagctg	312				
Db	121	catttggatactcaagattcctataagcagttag---gactcggagatggtatactcaagct	177				
QY	313	tattactctggacaatctggtggaataatataatgcacatgagctgagagctccctggccctacg	372				
Db	178	tactattctgcgccccttggttaataacaaatgcatatgctgtaaatctctggaaactctggaactgct	237				
QY	373	ttgagaggaactgtttgagccctcttggccggaacatttactcttgaagaacggttgaatgta	432				
Db	238	ttggaagagactgtttgactctgtgctggaagaacatttcccttaaaacagcttccatgta	297				
QY	433	gccacacgcagctgtcttctgcgaatggaataatgctcacttcaaaagaacctcaattaccgagat	492				
Db	298	gctatacacactgattctctgcagtggaataatgctcatctcaataagaacttgatataacgagat	357				
QY	493	gtcaagccagaagaactctctctgattgtgctgacaaaggcaataagaagaagacatgatatcac	552				
Db	358	gtaaaacctggaactctcttaataatagagaccaggaacaaacccagaaagatttctaac	417				
QY	553	attatagactttggaactgcggccaaagaaatattggaaccccgaaacccaaaaaacacatctc	612				
Db	418	attatagatttctgttcttggtgcaaaagaaatataatgtaacggaagacaaagaataacatac	477				
QY	613	tataggggaacacaaagaatttaactgcgaactgcgaagaataatgtctatcaacacagcatctt	672				
Db	478	tacagagacacccaaagagccttaccaggaacagcagatataatgagcataaacacacattta	537				
QY	673	ggcaaaagacaaagccggagagaatgatttggaaagcccttgagccatagtctcatgttcatcttc	732				
Db	538	ggaaaaagacaagaatagaaagacgaatttagaagcttttagaactatgttcaatgttcaatctt	597				
QY	733	cttcgaagcagctccctctggtgcaagaactcaagcctgcacacattaaagagagatataca	792				
Db	598	ctgagagagcagcttctccctcttgcaagcgttctaaagtttgcacacattaaagagagagatacag	657				
QY	793	aaaattgtgtgacacaaagaagaataactcccatgtgaagctcctctgcgaagaacttccagag	852				
Db	658	aaaattgtgagatacaaaaacgggtctaccaccaatagaagtgttatgtggaataatttcca---	714				
QY	853	gagatggaacctacactctgcataatgttcaaggcagctggaactcttctgaaaaacctgatat	912				
Db	715	gaaatggaacatactcttctgttatgtaagaagctagatttttttgaaaaaaccagaactat	774				
QY	913	gagattttaaggacctcttcaacagacactttttgaaaagaagaagctctacacactttgacctat	972				
Db	775	gactacttaagaagaagcttcttactgactatcttggacgcgaagaagagatatagtttgatatat	834				
QY	973	gacctatgttgggttggagagaccattctcactccagatgggttcaagttcaagttacatctc	1032				
Db	835	gaatatgctggtatctgtgtaaaacagttgctcattcccaagtggtgagcagttcagaagaatctc	894				
QY	1033	ggtgatactgtcaataactcgaaaagccacacacataaggatctggccatcacacaacagcag	1092				
Db	895	gctctgtcatcaaca---gagaagacacatcaacacagagataagttgcaacaatccaa-	950				
QY	1093	ccctctgcaaatcagctggttgaactcaacaaatggagagctgaaagtgtgatatcccaag	1152				

CC polynucleotides can be used as a source of primers and probes, which can
 CC be used for a variety of purpose, e.g. detection of expression levels,
 CC mapping, tissue typing or profiling, forensics, genetic analysis and
 CC detection of polymorphisms. Polypeptides encoded by the polynucleotides
 CC can be used for raising antibodies for experimental, diagnostic and
 CC therapeutic purposes. The polynucleotides may also be used to construct
 CC arrays for diagnostics (which may be used to determine function of an
 CC encoded protein); and to detect differences in expression levels of an
 CC two cells (e.g. to identify abnormal or diseased tissue in a human, to
 CC identify a genetic predisposition or susceptibility to a disease such as
 CC cancer). The polynucleotides of the invention are especially used in the
 CC diagnosis, prognosis and management of colorectal cancer, breast cancer,
 CC and lung cancer. The polynucleotides can also be used to screen for
 CC peptide analogues and antagonists.

50 Sequence 447 BP; 129 A; 106 C; 106 G; 104 T; 2 other;

Query Match 25.8%; Score 327.4; DB 20; Length 447;
 Best Local Similarity 96.8%; Pred. No. 1.8e-92;
 Matches 365; Conservative 1; Mismatches 7; Indels 4; Gaps 3;

QY 769 gaccattaaagagagatcaaaaatgtgacacccaagaagatcccatgaa 828
 |||||||
 Db 1 gacacattaaagagagatcaaaaatgtgacacccaagaagatcccatgaa 60
 QY 829 gctctctgagacattccagagagatgcaacctaccctgatatgagcgactg 888
 |||||||
 Db 61 gctctctgagacattccagagagatgcaacctaccctgatatgagcgactg 120
 QY 889 gactctttgaaaaacctgattatgattacagacccctctccagaccccttga 948
 |||||||
 Db 121 gactctttgaaaaacctgattatgattacagacccctctccagaccccttga 180
 QY 949 aagaagagctacaccttgatcagccatgattggtgtggaagacccctaccatca 1008
 |||||||
 Db 181 aagaagagctacaccttgatcagccatgattggtgtggaagacccctaccatca 240
 QY 1009 gtaggagtcagtcagcga-gattctgtgtcatctgcaatactcgagaagccacaca 1067
 |||||||
 Db 241 gtaggagtcagtcagcga-gattctgtgtcatctgcaatactcgagaagccacaca 300
 QY 1068 taggagtcgacatcaacaacagcagcctctcg--aatcaggtgtgtagctacaacat 1125
 |||||||
 Db 301 taggagtcgacatcaacaacagcagcctctcgaaatcaggtgtgtagctacaacat 360
 QY 1126 -ggagagctgaattgtg 1141
 |||||||
 Db 361 ggagagagctgaattgtg 377

RESULT 14
 AAC48459
 ID AAC48459 standard; DNA: 1407 BP.

XX AAC48459;

DT 18-OCR-2000 (first entry)

DE Arabidopsis thaliana DNA fragment SEQ ID NO: 57558.

XX Hybridisation assay; genetic mapping; gene expression control;

KW protein identification; signal transduction pathway;

XX metabolic pathway; promoter; termination sequence; ss.

OS Arabidopsis thaliana.

XX EPI033405-A2.

XX 06-SEP-2000.

PF 25-FEB-2000; 2000EP-0301439.

PR 25-FEB-1999; 99US-0121825.
 PR 05-MAR-1999; 99US-0123180.
 PR 09-MAR-1999; 99US-0123548.
 PR 23-MAR-1999; 99US-0125788.
 PR 25-MAR-1999; 99US-0126254.
 PR 29-MAR-1999; 99US-0126785.
 PR 01-APR-1999; 99US-0127462.
 PR 06-APR-1999; 99US-0128293.
 PR 08-APR-1999; 99US-0128714.
 PR 16-APR-1999; 99US-0129845.
 PR 19-APR-1999; 99US-0130077.
 PR 21-APR-1999; 99US-0130449.
 PR 23-APR-1999; 99US-0130510.
 PR 23-APR-1999; 99US-0130891.
 PR 28-APR-1999; 99US-0131449.
 PR 30-APR-1999; 99US-0132048.
 PR 30-APR-1999; 99US-0132407.
 PR 04-MAY-1999; 99US-0132484.
 PR 05-MAY-1999; 99US-0132485.
 PR 06-MAY-1999; 99US-0132486.
 PR 07-MAY-1999; 99US-0132487.
 PR 07-MAY-1999; 99US-0132863.
 PR 11-MAY-1999; 99US-0134256.
 PR 14-MAY-1999; 99US-0134218.
 PR 14-MAY-1999; 99US-0134219.
 PR 14-MAY-1999; 99US-0134221.
 PR 14-MAY-1999; 99US-0134370.
 PR 18-MAY-1999; 99US-0134768.
 PR 19-MAY-1999; 99US-0134941.
 PR 20-MAY-1999; 99US-0135124.
 PR 21-MAY-1999; 99US-0135353.
 PR 24-MAY-1999; 99US-0135629.
 PR 25-MAY-1999; 99US-0136021.
 PR 27-MAY-1999; 99US-0136392.
 PR 28-MAY-1999; 99US-0136782.
 PR 01-JUN-1999; 99US-0137222.
 PR 03-JUN-1999; 99US-0137528.
 PR 04-JUN-1999; 99US-0137502.
 PR 07-JUN-1999; 99US-0137724.
 PR 08-JUN-1999; 99US-0138094.
 PR 10-JUN-1999; 99US-0138540.
 PR 10-JUN-1999; 99US-0138847.
 PR 14-JUN-1999; 99US-0139119.
 PR 16-JUN-1999; 99US-0139452.
 PR 17-JUN-1999; 99US-0139453.
 PR 17-JUN-1999; 99US-0139459.
 PR 18-JUN-1999; 99US-0139454.
 PR 18-JUN-1999; 99US-0139455.
 PR 18-JUN-1999; 99US-0139456.
 PR 18-JUN-1999; 99US-0139457.
 PR 18-JUN-1999; 99US-0139458.
 PR 18-JUN-1999; 99US-0139459.
 PR 18-JUN-1999; 99US-0139460.
 PR 18-JUN-1999; 99US-0139461.
 PR 18-JUN-1999; 99US-0139462.
 PR 18-JUN-1999; 99US-0139463.
 PR 18-JUN-1999; 99US-0139750.
 PR 18-JUN-1999; 99US-0139751.
 PR 21-JUN-1999; 99US-0139817.
 PR 22-JUN-1999; 99US-0139899.
 PR 23-JUN-1999; 99US-0140353.
 PR 23-JUN-1999; 99US-0140354.
 PR 24-JUN-1999; 99US-0140695.
 PR 28-JUN-1999; 99US-0140823.
 PR 29-JUN-1999; 99US-0140991.
 PR 30-JUN-1999; 99US-0141287.
 PR 01-JUL-1999; 99US-0141642.
 PR 01-JUL-1999; 99US-0142154.
 PR 02-JUL-1999; 99US-0142055.
 PR 06-JUL-1999; 99US-0142390.
 PR 08-JUL-1999; 99US-0142803.
 PR 09-JUL-1999; 99US-0142920.
 PR 12-JUL-1999; 99US-0142977.

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 17, 2002, 20:23:16 ; Search time 50.12 Seconds
(without alignments)
6219.252 Million cell updates/sec

Title: US-09-765-068-1
Perfect score: 1269
Sequence: 1 atgaccatctagtagga.....ctgcacgcacaaatga 1269

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 38353 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 10%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/lna/5A.COMB.seq:*
2: /cgn2_6/ptodata/1/lna/5B.COMB.seq:*
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4: /cgn2_6/ptodata/1/lna/6B.COMB.seq:*
5: /cgn2_6/ptodata/1/lna/CTOS.COMB.seq:*
6: /cgn2_6/ptodata/1/lna/Dackfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	608.8	48.0	2405	1	US-08-454-097-30 Sequence 30, Appl
2	608.8	48.0	2405	3	US-08-185-359-30 Sequence 30, Appl
3	564.8	44.5	1233	1	US-08-454-097-32 Sequence 32, Appl
4	564.8	44.5	1233	3	US-08-185-359-32 Sequence 32, Appl
5	279.6	22.0	3505	1	US-08-454-097-34 Sequence 34, Appl
6	279.6	22.0	3505	1	US-08-468-036-43 Sequence 43, Appl
7	279.6	22.0	3505	2	US-08-376-843-43 Sequence 43, Appl
8	279.6	22.0	3505	2	US-08-185-359-34 Sequence 34, Appl
9	267.8	21.1	1210	1	US-08-447-500-7 Sequence 7, Appl
10	267.8	21.1	1210	1	US-08-454-097-7 Sequence 7, Appl
11	267.8	21.1	1210	1	US-08-453-866-7 Sequence 7, Appl
12	267.8	21.1	1210	3	US-08-185-359-7 Sequence 7, Appl
13	267.8	21.1	1779	1	US-08-447-500-9 Sequence 9, Appl
14	267.8	21.1	1779	1	US-08-453-866-9 Sequence 9, Appl
15	267.8	21.1	2914	3	US-08-454-097-11 Sequence 11, Appl
16	267.8	21.1	2914	3	US-08-185-359-11 Sequence 11, Appl
17	262.2	20.7	2468	1	US-08-468-036-19 Sequence 19, Appl
18	262.2	20.7	2468	2	US-08-376-843-19 Sequence 19, Appl
19	262.2	20.7	2469	1	US-08-447-500-3 Sequence 3, Appl
20	262.2	20.7	2469	1	US-08-454-097-3 Sequence 3, Appl
21	262.2	20.7	2469	3	US-08-453-866-3 Sequence 3, Appl
22	262.2	20.7	2469	3	US-08-185-359-3 Sequence 3, Appl
23	237.4	18.5	1520	3	US-09-100-664A-1 Sequence 1, Appl
24	234.2	18.5	1485	1	US-08-468-036-8 Sequence 8, Appl
25	234.2	18.5	1485	2	US-08-376-843-8 Sequence 8, Appl
26	234.2	18.5	3098	1	US-08-447-500-1 Sequence 1, Appl
27	234.2	18.5	3098	1	US-08-454-097-1 Sequence 1, Appl

28	234.2	18.5	3098	1	US-08-447-408-1 Sequence 1, Appl
29	234.2	18.5	3098	1	US-08-453-866-1 Sequence 1, Appl
30	234.2	18.5	3098	3	US-08-185-359-1 Sequence 1, Appl
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34	225.2	17.7	1989	3	US-08-185-359-5 Sequence 5, Appl
35	195.4	15.4	1689	1	US-08-447-500-11 Sequence 11, Appl
36	195.4	15.4	1689	1	US-08-453-866-11 Sequence 11, Appl
37	195.4	15.4	2385	1	US-08-454-097-9 Sequence 9, Appl
38	195.4	15.4	2385	1	US-08-468-036-41 Sequence 41, Appl
39	195.4	15.4	2385	2	US-08-376-843-41 Sequence 41, Appl
40	195.4	15.4	2385	3	US-08-185-359-9 Sequence 9, Appl
41	162.8	12.8	3627	1	US-08-447-500-23 Sequence 23, Appl
42	162.8	12.8	3627	1	US-08-454-097-23 Sequence 23, Appl
43	162.8	12.8	3627	1	US-08-453-866-23 Sequence 23, Appl
44	162.8	12.8	3627	3	US-08-185-359-23 Sequence 23, Appl
45	162.8	12.8	3628	1	US-08-468-036-17 Sequence 17, Appl

ALIGNMENTS

RESULT 1
US-08-454-097-30
Sequence 30, Application US/08454097
Patent No. 5686412
GENERAL INFORMATION:
APPLICANT: Hoechst, Merl F.
TITLE OF INVENTION: Protein Kinases
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
SECRET: 233 South Wacker Drive, 6300 Sears Tower
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,097
FILING DATE: 30-MAY-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/185,359
FILING DATE: 21-JAN-1994
APPLICATION NUMBER: US 08/008,001
FILING DATE: 21-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/728,783
FILING DATE: 03-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: No. 5686412and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/31853
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 2405 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 67..1197


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QY 193 tacaccaatgaatatgtatgaatcaactggaaccataataatcaatgctcccaagctt 252
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Db 238 TTGGAGAGCTTTGTGACTGTGTGACAGACATTTTCTTAAACAGCTTCTCATGATA 297
QY 433 gccacccagctctctctggaatggaatggaatggaatggaatggaatggaatggaat 492
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QY 493 gtaacagcagagaactctctgcatggtgcagacaggaacaaataagaagacatgtatacac 552
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QY 913 gagatattgaagacccctctcaagacactcttgaaagaaagccttgaactat 972
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QY 1033 ggttcattctgaataactcgaagaagcacaacataagagatcgagccacacagagag 1092
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QY 1213 aagtgctgctgttctcttaagagg 1236
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RESULT 4
US-08-185-359-32
; Sequence 32, Application US/08185359
; Patent No. 6060296
; GENERAL INFORMATION:
; APPLICANT: Hoechst, Merl F.
; TITLE OF INVENTION: Protein Kinases
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive, 6300 Sears Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/185,359
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/008,001
; FILING DATE: 21-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/728,783
; FILING DATE: 03-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6060296and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 27866/31853
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1233 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1041
; US-08-185-359-32

Query Match 44.5%; Score 564.8; DB 3; Length 1233;
Best Local Similarity 72.7%; Pred. No. 2.6e-173;
Matches 803; Conservative 0; Mismatches 282; Indels 19; Gaps 5;

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QY 313 tattacttgagacatlglyggaataataatgcatlglygtgagctctcttgccctaac 372
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||||| 238 TTGAAGACTGTTGACTTGTGACAGAAACATTTCTTAACAGTTCATGATA 297
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DB 298 GCTATACAACTGATTTCCGATGGAATATGTCCATCAAGAACTGATATACAGAGAT 357
QY 493 gtcaagccaggaactctcgtgattgtgcgaaagcaataaggaaggcattatcac 552
DB 358 GTAAACCTGAACTCTTATATAGAGACGACAGAAACAAACCCCAAGATTATTCAC 417
QY 553 attatgactcttgagctgagcaagaaatatactgaccccgaaacaaacacatacct 612
DB 418 ATTATAGTTTGGTTGGCAAAAGAAATATATATATCCGGAGCAAAAGAAACATATACA 477
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DB 478 TACAGAGAACACAGAGAGCCTTACAGAAACAGCTAGATATATAGACATTAACACATTTA 537
QY 673 ggcacaaagacaaagccgagagatgattggaagccctaggccatgctatgctatctt 732
DB 538 GGAAGAAGCAAAAGTAGAAGAGAGAGATTAGAACCTTTAGCTCATATGTTATGTAATTT 597
QY 733 ctccagagcaagccctccctgcaagagactcaagcgtgacacattaaagagagatcaaa 792
DB 598 CTGAGAGGACATCTTCTTGGCAAGCCTTAAGTTGACATTAAGTAAGAGAGATACAG 657
QY 793 aaattggtgacacacaaaggaatactccatcgaagctctcgtgagaaactccagag 852
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QY 973 gactatgattggttggagagacactatccctactccatgagtgagtgatcagtgatctt 1032
DB 835 GAATATGACTGATGTTGTAAGAAAGTGTGCTACTCCAGTGGTGAGTTGACAGAGATCT 894
QY 1033 ggtgcatcgtgaataactcgcggaagacacacatagggatgagccatccacacagcag 1092
DB 895 GCTGTGATATAACA---GAGAAAGCAATGACACAGAGATAAGATGCAACATTCACAA- 950
QY 1093 cctctcgaacatcaggtggttagctcaacaaatgagagcgtgaatgttgaatcccaag 1152
DB 951 -----AAMCCAGGTTGTAAAGTTCTAACAATGAGAGTTAAACACAGATGACCCACC 1002
QY 1153 ggaagcccaatcaatgcaacaaatcagacgtcgaatgaggtgaggtgaggtgaggaagct 1212
DB 1003 GCAG-ACGTTCAAAATGCAACCATCACAGCCCTACTGTAAGTAAGAAAGATGATGAGAAAC 1061
QY 1213 aagtcgtcgtcttcttaagagg 1236
DB 1062 AACTGCCAGAAAGTGTGACATG 1085

RESULT 5
US-08-454-097-34
Sequence 34. Application US/08454097
Patent No. 5686412
GENERAL INFORMATION:
APPLICANT: Hoechst, Merl F.
TITLE OF INVENTION: Protein Kinases
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borum
STREET: 233 South Wacker Drive, 6300 Sears Tower
CITY: Chicago
STATE: Illinois

COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,097
FILING DATE: 30-MAY-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/185,359
FILING DATE: 21-JAN-1994
APPLICATION NUMBER: US 08/008,001
FILING DATE: 21-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/728,783
FILING DATE: 03-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: No. 5686412and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/31853
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 3505 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 154..1398
US-08-454-097-34
Query Match 22.0%; Score 279.6; DB 1; Length 3505;
Best Local Similarity 58.9%; Pred. No. 1.9e-80;
Matches 521; Conservative 0; Mismatches 354; Indels 9; Gaps 2;
QY 101 cctctgggtgtcttattggttgagaccactcaggttgggaagaagatagatgagga 160
DB 149 CCGCATGAGCTGAGAGTGGGAAACAGTACCGGCTGGCCGGAAGTCCGACGGCT 208
QY 161 actcggagagctcagattaggtlaaaaaatctacacaaatgaaatagaaatcaaac 220
DB 209 CTTGCGAGACATCTATCTCGGTGCGGACATTTGCTGCAGAGAAAGAGGTTCCATCAAC 268
QY 221 tggaaaccaataaatacaagctgctcacaagctcaatlttagagtaagattataaacagc 280
DB 269 TTGAATGTGTCAAAACCAACCAACCTCAGCTCCACATTTGAAGAGCAAAATCTACA---AGA 325
QY 281 ttggcaatgcaagtggaaggtctcccaagagtgattacttggaccatgtyggaataata 340
DB 326 TGATGACAGGAGAGAGTGGGATCCCAACATACATAGTGTGGGGGCAAGAGGGGACATACA 385
QY 341 atgcacatgctcagagctccttgccctagcttgaggaagactgttgaacctcgtgacc 400
DB 386 ACGTCATGTGATGTGACCTGCTGGGCGCAAGCTGAGAGACCTTCAACTTCTGCTCCA 445
QY 401 gaacattacttgaagaaggtgttaatgataagccatcccaagctcttctgaaatgaat 460
DB 446 GGAATTCAGGCTTCAAAACCGCTCTGCTGCTGCTGCTGCAACCAATATAGTGCATCAAT 505
QY 461 acgtgcacaaagaacactattacagagatgcaagagagaaacttccctgattgttc 520
DB 506 ACATTCATTCAAAGAACTTCTTCACCGGGGATGGAAGCCAGAAACATCTCTCATGGGCC 565
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Db 566 -----TGGGGAAGAGGCGAACCTGGTGTACATCACTTCGGGGCTGGCCAAAGCT 619
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RESULT 6
US-08-468-036-43
: Sequence 43, Application US/08468036
: Patent No. 5728806
: GENERAL INFORMATION:
: APPLICANT: Demaggio, Anthony J.
: APPLICANT: Hoeksma, Merl F.
: TITLE OF INVENTION: Materials and Methods Relating to Proteins that
: INTERACT WITH CASEIN KINASE I
: NUMBER OF SEQUENCES: 48
: CORRESPONDENCE ADDRESS:
: ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borum
: STREET: 6300 Sears Tower, 233 South Wacker Drive
: CITY: Chicago
: STATE: Illinois
: COUNTRY: United States of America
: ZIP: 60606-6402
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/468 036
: FILING DATE: 06-JUN-1995
: CLASSIFICATION: 530
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/184,605
: FILING DATE: 21-JAN-1994
: ATTORNEY/AGENT INFORMATION:
: NAME: NO. 5728806and, Greta E.
: REGISTRATION NUMBER: 35,302
: REFERENCE/DOCKET NUMBER: 27866/31784
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 312/474-6300
: TELEFAX: 312/474-0448
: TELEX: 25-3856
: INFORMATION FOR SEQ ID NO: 43:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 3505 base pairs
: TYPE: nucleic acid

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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-468-036-43

Query Match      22.0%; Score 279.6; DB 1; Length 3505;
Best Local Similarity 58.9%; Pred. No. 1.9e-80;
Matches 521; Conservative 0; Mismatches 354; Indels 9; Gaps 2;

QY 101 cctctgggttcttatgtgtgggaccccaacttaaggttggcaagaagatagatgtgga 160
Db 149 CCGCATGGAGCTGAGAGTGGGAAACAGGTACCGGCTGGCGGAGAAATGCGACCGCT 208
QY 161 acttggagagctcagattaggttaaaatcttaccacccatgaatcagtagaacaac 220
Db 209 CCTTGGAGACATCTATCTCGGTAGGACATTGCTGAGAGAAAGATGTCCATCAAGC 268
QY 221 tggaaaccaataaatacagtgctcacaagcttcaatttagatagacagatttaaacagc 280
Db 269 TTGAATGTGTCAAAACCAAAACCCCTGACCTCCACATTGAGAGCAAAATCTACA--AGA 325
QY 281 ttggcagtgaggtgaaaggtctcccaaggtgattactttggaccatgtggaatata 340
Db 326 TGATCGAGGAGAGAGTGGGCAATCCACCATGAGATGTGGGGGCGAGAGGGGACTACA 385
QY 341 atgcacatgtgtgtgagctccttggcccttagcttggagagctgttgaacctgtgacc 400
Db 366 ACGTATGTGATGAGAGCTGCTGGGGCCAGCGCTGGAGAGCTCTTCAACTTCTCTCCA 445
QY 401 gaacattacttgaagaagtgtaatagtatagccatccagctgtcttcgaaatgaaat 460
Db 446 GGAATTCAGCCTCAAAACCCGCTGCTGTGTGACCAATGATGATGCGATCAAT 505
QY 461 acgtgactcaagaacactcattaccagatgttaacccagagagacttctgtatgttc 520
Db 506 ACATTCAATCAAAAGACTCATTCACCGGGAGTGAACCCAGACAACTCTCATAGGGCC 565
QY 521 gacaagcaataaagaagaagcatgttatacattatagacttggacttggccaaagaaat 580
Db 566 -----TGGGGAAGAGGCGAACCTGGTGTACATCACTTCGGGGCTGGCCAAAGCT 619
QY 581 acattgacccgaaacaaacacataccttataggaacaaagttaactggaa 640
Db 620 ACCGGATGACAGCAACCCACGACATCCCTATGTGAGAAAGAAACCTCACGGGGA 679
QY 641 ctgcaagatatatgtctatcaacacgcatcttggcaagaacgaggaagatgatt 700
Db 680 CCGCGGGGTACCGCTCCATCAACACGCACTTGAATTGAACATCCCAAGAGATGACT 739
QY 701 tggagagccctaggccatcgttcacgttatcttcttggagcagccctctggcaagac 760
Db 740 TGGAGCTCTTGGGCTACGTGCTAAATGTAATCACTGGGGCTCTCCCTGGCAGGGCT 799
QY 761 tcaagctctacacatlaaagagagatatacaaaaattgtgtgacacaaagaataacc 820
Db 800 TGAAGCTGCGCCACCAAGACAGAAATACGAAGATTTCGCAAGAAATGTCCACCC 859
QY 821 ccattgaagctctctgtgagaaacttccagagagagatggcaacctactcgatgtca 880
Db 860 CCATGGAAGTGTGTAAAGGCTACCCCTCCGAATTGGCCACATACCTGAATTTCTGCC 919
QY 881 ggcagctgactctcttgaanaaactgattatgattattacagaccccttcacagacc 940
Db 920 GTTCCTTGCGTTTACGACGACAGCCTGACTACTCGTACCTGGCGAGCTTTCCGGATC 979
QY 941 tcttgaanaaagaagctacaccttgaactatgcatgattatgg 984
Db 980 TGTTCATCGCCAGGCGTTCTCTATGACTAGCTGTTCGACTGG 1023

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RESULT 7
US-08-376-843-43

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DB 371 CTTAAGGTGGGTT---GGCATCCCCACATACGAGTGTGTCAGAAAAAGACTAC 427
QY 340 aatgcattgctgagagctccttgccctagcttgaggaacttgcttgacctgtgac 399
DB 428 AATGTACTAGCATGATCTTCTTGAGACTGACCTCGAAGCCCTTCAATTTCTGTCA 487
QY 400 cgaacattacttgaagcagtgtaataatgataagcaccagctgtcttcgaaatgaa 459
DB 488 AGAAGGTTCAACATGAAGAACTGTAATGTTAGTCTGACCGAGATGATGAGTAATGAA 547
QY 460 taactgcaactaaagaacctattaccgagatgtaacgcaaggaacttctgattgt 519
DB 548 TATGTGCATACAAAGAAATTTTATACAGACACATTAACCAATTAATCTGATGGT 607
QY 520 cgaacagcaataaagaagacatgatatatacatattagacttgactgccaagaa 579
DB 608 ATTGGGGCTACCTGTAATAG-----TTATTCCTTATGATTTTGGTTGGCCAAAAG 661
QY 580 tacattgaaccgccgaacaaacacacatactataggggaacaaagttaactgga 639
DB 662 TACAGAGACAACAGACAGCAACATACATACAGAGAAATAAACCTCAGCTGCG 721
QY 640 actgcaagatatatgctataacacagcatcttgcaagaagcaagccgagagatgat 699
DB 722 ACTGCCGATATGCTTACATCAATGACATCTGTGATGAGCAGACTCGCCGAGATGAC 781
QY 700 ttggaagcccaagacatattgcatatttctctgaggaagcccccctgcaagaa 759
DB 782 ATGAAATCATATAGATATGTTTATGATTTTAAAGAACCCCTGCGCATGCAAGG 841
QY 760 ctcaagctgcacataaagaagagataatcaaaaaatltggtgacacaaagaact 819
DB 842 CTAAAGCTGCACAAAGAAACAAATATGAAAGATAGTAAAGATGTCCACG 901
QY 820 cccattgaagctctctggaagacttccagagagatggaacctactctgatatg 879
DB 902 CCTTTAAGTTTATGTAAGGGGTTCTCGAAGTTTGGAATTTAACTAATGTT 961
QY 880 aggaagctgagactctctggaagacccgatatgattatgaagccctctcacagac 939
DB 962 CGTGGGCTACCTTTGAAGAAAGCCCGCATATGATGATGAGAGCAGCTTTCGCAT 1021
QY 940 ctcttgaagaagaagctacacacttgactgactgactgattgg 984
DB 1022 CTTTACAGACCTGAAACATCATATGACTACACATTTGATTGG 1066

RESULT 10
US-08-454-097-7
Sequence 7, Application US/08454097
Patent No. 5686412
GENERAL INFORMATION:
APPLICANT: Hoechst, Merl F.
TITLE OF INVENTION: Protein kinases
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sears Tower
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/454,097
FILING DATE: 30-MAY-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/185,359
FILING DATE: 21-JAN-1994
APPLICATION NUMBER: US 08/008,001
FILING DATE: 21-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/728,783
FILING DATE: 03-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: No. 5686412and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/31853
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1210 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
IMMEDIATE SOURCE:
CLONE: Protein Kinase
FEATURE:
NAME/KEY: CDS
LOCATION: 173..1147
US-08-454-097-7

Query Match 21.18; Score 267.8; DB 1; Length 1210;
Best Local Similarity 58.18; Pred. No. 6.6e-77;
Matches 514; Conservative 0; Mismatches 362; Indels 9; Gaps 2;

QY 100 tccctcgtgggtcttctatgctgagagcccaactcaggggttgcaagaagatagatgag 159
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QY 160 aactcggagagctcagattagtaaaatctctacacaaatgaatatgtagaatcaa 219
DB 251 TCCATTGGGAGCATCTATTGCGGATCACTACCAACGCGGAGAAAGTGCGAGTGA 310
QY 220 ctggaaccaataaataacagtgctcccaagcttattatgagtgatgagatttaaaag 279
DB 311 CTGAATCTCAGAAAGGCGAGGATCCCAAGTTGCTGACGAGACAGCTCTATTAAGATT 370
QY 280 ctgagcagtgcaagtggaagctctcccaagtgatattacttgagcaatgaggaatat 339
DB 371 CTTCAAGGTGGGTT---GGCATCCCCACATACGATGATGATGTCAGAAAAAGACTAC 427
QY 340 aatgcattgctgagagctccttgccctagcttgaggaacttgcttgacctgtgac 399
DB 428 AATGTACTAGCATGATCTTCTTGAGACTGACCTCGAAGCCCTTCAATTTCTGTCA 487
QY 400 cgaacattacttgaagcagtgtaataatgataagcaccagctgtcttcgaaatgaa 459
DB 488 AGAAGGTTCAACATGAAGAACTGTAATGTTAGTCTGACCGAGATGATGAGTAATGAA 547
QY 460 taactgcaactaaagaacctattaccgagatgtaacgcaaggaacttctgattgt 519
DB 548 TATGTGCATACAAAGAAATTTTATACAGACACATTAACCAATTAATCTGATGGT 607
QY 520 cgaacagcaataaagaagacatgatatatacatattagacttgactgccaagaa 579
DB 608 ATTGGGGCTACCTGTAATAG-----TTATTCCTTATGATTTTGGTTGGCCAAAAG 661
QY 580 tacattgaaccgccgaacaaacacacatactataggggaacaaagttaactgga 639
DB 662 TACAGAGACAACAGACAGCAACATACATACAGAGAAATAAACCTCAGCTGCG 721
QY 640 actgcaagatatatgctataacacagcatcttgcaagaagcaagccgagagatgat 699
DB 722 ACTGCCGATATGCTTACATCAATGACATCTGTGATGAGCAGACTCGCCGAGATGAC 781

QY 700 ttgagaagcccaaggccatcttcattatcttccttgagcaagccccccttgcaaga 759
Db 782 ATGGAATCATTTAGCATATGTTTATGTATTTTAAATGAACCAAGCCCGCATGGCAAGG 841
QY 760 ctcaagagctgcacattaaaagagatatacaaaaatctggtagcccaaaagaaact 819
Db 842 CTAAAGGCTGCACAAAGAAAACAAAATATGAAAAAGTTAGTGAAAAAGAAAGTCCACG 901
QY 820 cccattgaagctctcttgagaacttccagagagatgcaacactccttgatagtc 879
Db 902 CCTGTGAAGTTTATGTGAAGGGTTTCCCTGCAGAAATTTGCGATGTRCTTAACTATTG 961
QY 880 aggcgaactggaactctcttgaaaaaacctgattatgattatlaaggaacctcaccagac 939
Db 962 CGTGGCGTACCCCTTTGAGGAAGCCCCAGATTACATGATCTGTGAGGCAAGCATTTCCGCATT 102
QY 940 ctctcttgaaaagaaggctacacacttgactgattgacatgatgsg 984
Db 1022 CTTTTCAGAGCCCTGAACCATCATATATGACTACACATTTTATATGG 1066

RESULT 11

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US-08-453-866-7
Sequence 7, Application US/08453866
Patent No. 5756289
GENERAL INFORMATION:
APPLICANT: Hoekstra, Merl F.
TITLE OF INVENTION: PROTEIN KINASES
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East, Suite 500
CITY: Los Angeles
STATE: CA
COUNTRY: USA
ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/453,866
FILING DATE: 30-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/008,001
FILING DATE: 20-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Wetherell Ph.D., John R.
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: PD-2458
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
INFORMATION FOR SEQ. ID NO. 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1210 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
IMMEDIATE SOURCE:
CLONE: Protein Kinase
FEATURE:
NAME/KEY: CDS
LOCATION: 173..1147
US-08-453-866-7

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Query Match	21.1%;	Score 267.8;	DB 1;	Length 1210;
Best Local Similarity	58.1%;	Pred. No. 6.8e-77;		

Matches	514;	Conservative	0;	Mismatches	362;	Indels	9;	Gaps	2;
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QY	160	aactcggagagcgcagattaggttaaanaatcttaacccaataaataatagaaatcaaa		219					
Db	251	TCCCTTCGGGACATCTATTGGCGATACATACACACGCGCAAGGAAAGGGAGTGAAG		310					
QY	220	ctggnaaccaaataatcacgtgtctccacagcttcattagtagacagattataaacag		279					
Db	311	CTAGAAATCTAGAAAGGCCAGCATCCCCAGTCTCTGTAGAGAGCAAGCTCATAGATT		370					
QY	280	cttgcgcagtgccaggtgaaggtctccacagtgatlaacttggacatgtggaatat		339					
Db	371	CTTCAAGGTGGGGT---GGCATCCCCACATACGGGTGGTATGGTCAGAGAAAAGACTAC		427					
QY	340	aatgcacatgtctgtagagctcccttgccctagcttggagaactgtgttgaactctgtac		399					
Db	428	AAATGTAATCATATGAGATCTTCTGGAGACCTAGCGCTGGAAGACCTCTCAATTCATGTTCA		487					
QY	400	cgaacattactcttgtaagaacggtgttaatatagacacacagctgtcttcctgaattgaa		459					
Db	488	AGAAAGTTCACATGAAACCTGTACTTATGTATGCTGACCAATGATCATGTAATTGAA		547					
QY	460	taegtgaactcaagaacacctcaattcacagagatgtcaaacccagagaaactctcgtatgt		519					
Db	548	TATGTGCATCAAAAGAAATTTTATACACAGAGACATTAACCAAGATTAATCTTAATGGGT		607					
QY	520	cgaacagcgaataagaagaagcagtgtataacacattatagaacttggagcttggagccaagaa		579					
Db	608	ATTGGGCGTCACTGTATAAG-----TTATTCCTTATTTGATTTGGTTGGCCAAAAG		661					
QY	580	tacattaccoccgaaaccaaacaacatcaccttaagtaggaacacaaagtttaactga		639					
Db	662	TAAAGAGACAAACAGGCAAGGCAACACATACCTACAGGAAGATTAACCTCACTGGC		721					
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QY	700	ttagaagccctagggccatatgttcaatgattctcccttgaggagagctcccccggaaaga		759					
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QY	760	ctaaagcgcaacacattaaagagagatactcaaaaatgtgtgcagaccaaaagaaactact		819					
Db	842	CTTAAGGCTGCAACAAGAAACAAATATGAAAAGATTAGTGAAGAAAGATGTCACG		901					
QY	820	cccaatggaagctctcgttagaagacttccaagagagatgtgcacaccttaccctgatgtc		879					
Db	902	CCGTGTAAGATTTTATGTAAGGGGTTTCTCGAGATTTGCCATGTACTTAACATATGT		961					
QY	880	aggcgacitggaactcttgaanaaaactgtatcttgatcttaacggaaacctcttcacagac		939					
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RESULT

US-08-185-359-7
Sequence 7, Application US/08185359
Patent No. 6060296
GENERAL INFORMATION:
APPLICANT: Hoekstra, Merl F.
TITLE OF INVENTION: Protein Kinases
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

```

STREET: 233 South Wacker Drive, 6300 Sears Tower
City: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/185,359
FILING DATE:
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/008,001
FILING DATE: 21-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/728,783
FILING DATE: 03-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: No. 6060296and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/31853
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1210 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
IMMEDIATE SOURCE:
CLONE: Protein Kinase
FEATURE:
NAME/KEY: CDS
LOCATION: 173..1147
US-08-185-359-7

Query Match      21.1%; Score 267.8; DB 3; Length 1210;
Best Local Similarity 58.1%; Pred. No. 6.8e-77;
Matches 514; Conservative 0; Mismatches 362; Indels 9; Gaps 2;

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Db 548 TATGTCATCAAAAGATTATTATACACAGACATTAAACCAGATTAATTCTAATGGCT 607
QY 520 cgacaagcacaataagaagcattgtatcacatratatagacttggacggccaagaa 579
Db 608 ATGGCGCTCAGTCTAATAAG-----TTATTCCTTAATTAATTTGGTTGGCCAAAAG 661
QY 580 tacattgacccgaaacaaacacatccttataggaacacaagaatttaactgga 639
Db 662 TACAGAGACACACAGACAGACAGACACATACATACAGAGAAGTAATAAACCCTCAGGC 721
QY 640 actgcaagatatagtctalcaacacgcattctggcaagaagaacggagagatgat 699
Db 722 ACTGCCCATATGCTAGCATCAATGCACATCTTGATATGAGCAGAGTCCCGCAGATGAC 781
QY 700 ttggaagccttagccatagttcatatgtatttcccttgagagccccccttgcaagga 759
Db 782 ATGGAATCATATTAGATATGTTTGATGTATTTAAATGAACACGCCCTGATGGCAAGGG 841
QY 760 ctcaagctcacacatataagaagagatatacaaaaattgtgacacacaagaataact 819
Db 842 CTAAAGGCTCCACAAAGAAACAAATATGAAGATTGTGAAGAAAGATGTCACG 901
QY 820 cccattgaagctctctgtggaacttccagagagatggcaacttgcatalgtc 879
Db 902 CCTGTTGAAGTTTATGTAAGGGGTTCTCGACAGAAATTCGATGTACTTAACATATTGT 961
QY 880 aggcgactgactcttcttgaaaaacctgattatagatattgaagacccttcacagac 939
Db 962 CGTGGCTACGCTTTGAGGAAGCCCAAGATTACATGTATGTGAGGCACTATTCCGATT 1021
QY 940 ctcttgaagaagaagctcaccttgactatgacctatgag 984
Db 1022 CTTTACAGACCTGAAACATCATATGACTACACATTTGATTCG 1066

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RESULT 13
US-08-447-500-9
Sequence 9, Application US/08447500
Patent No. 5627064
GENERAL INFORMATION:
APPLICANT: Hoechst, Merl F.
TITLE OF INVENTION: PROTEIN KINASES
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSER: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East, Suite 500
CITY: Los Angeles
STATE: CA
COUNTRY: USA
ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/447,500
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/008,001
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Wetherell Ph.D., John R.
REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: PD-2458
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1779 base pairs
TYPE: nucleic acid

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Db 518 AATTAAGTACGATGATCTTCTGAGCCTAGCCTCGAAGACCTTCAATTTGTGTCA 577
Qy 400 cgaacattacttgaagacggtgtaataagaccacacagctgcttcgaatgaa 459
Db 578 AGAAGTTCAACAAAGAACTGTAATGTTAGTACGACGAGATGATGAGTAATGAA 637
Qy 460 taatgacataaagaacatttaccagagatgtaacgaagaacttcctgattg 519
Db 638 TATGTGATACAAAGAAATTTATACAGAGACATTAACGATTAACCTCTATATGGT 697
Qy 520 cgaagaagcaataaagaagacatgataacatataagattgagcagcaagaa 579
Db 698 ATTGGGGCTCACTGTAATAG-----TTATCTTATTTGATTTGGTTGGCCAAAAG 751
Qy 580 tacattgaccccgaaacaaacacatacattatagggagacaaagttaactgga 639
Db 752 TACAGAGCAACAGAGCAACAGCAACATACCATACAGAGAAATAAACCTCAGTGGC 811
Qy 640 actgcaagataatgctatcaacacgcatcttgcaagaagacccggaagatgat 699
Db 812 ACTGCCGATATGCTACATCAATGACATCTTGTAATGAGAGATCGCCGAGATGAC 871
Qy 700 ttggaagccctgaagcacaatgatacttcttgcagagcagccctcctgcaagaa 759
Db 872 ATGGAATCATATTAGATATGTTTATGATGATTTATAGAACCACTGCTGAGCAAGG 931
Qy 760 ctcaagcctgacacattaaagagatacaaaaatltgtgacacaaagaataact 819
Db 932 CTAAAGGCTGCAACAAAGAAACAAATATGAAGATGTAAGAAAGATGTCACAG 991
Qy 820 ccaattgaagctctgtgtgagaccttcacagagagatgagacactcctgatatgc 879
Db 992 CCTGTGAAGTTATGATTAAGGGGTTCTGCAAGATTTGCGATGACTTAACATATTGT 1051
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Db 1052 CGTGGCTACCTTTGAGAGAGCCCGCAGATTAATCATGTAATGAGGACGCTATTCCGATT 1111
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Db 1112 CTTTTCAGAGCCCTGAGCAATCATATGACTACATGATTGTTGG 1156

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RESULT 15
 US-08-454-097-11
 ; Sequence 11, Application US/08454097
 ; Patent No. 5686412
 ; GENERAL INFORMATION:
 ; APPLICANT: Hoechst, Merl F.
 ; TITLE OF INVENTION: Protein Kinases
 ; NUMBER OF SEQUENCES: 57
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 ; STREET: 233 South Wacker Drive, 6300 Sears Tower
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: USA
 ; ZIP: 60606-6402
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/454,097
 ; FILING DATE: 30-MAY-1995
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/185,359
 ; FILING DATE: 21-JAN-1994
 ; APPLICATION NUMBER: US 08/008,001
 ; FILING DATE: 21-JAN-1993

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/728,783
; FILING DATE: 03-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5686412and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE NUMBER: 27866/31853
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2914 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 265..1275
; US-08-454-097-11

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Query Match 21.1%; Score 267.8; DB 1; Length 2914;
 Best Local Similarity 58.1%; Pred. No. 1.2e-76;
 Matches 514; Conservative 0; Mismatches 362; Indels 9; Gaps 2:

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Qy 100 tcccttggtgtcttactatgltggtgagcccaactcaggtgtgcaagaagatagatgtg 159
Db 283 TCCAGAGCTGATATCATTTGTCGAGGGAATATTAACGTGAGGAGATGGGTCTGCG 342
Qy 160 aactcagagagctcagattagtaaaatctcaacaaatgatatgtagcaataa 219
Db 343 TCCCTCGGGGCACTTATTTGGCGATCAATCAACCAACGCGAGAGTGGCGTGAAG 402
Qy 220 ctggaaccaataaataacagtgctccacagctcattatagagatagattataaag 279
Db 403 CTGAATCTCAGAGGCGAGGCAATCCCGAGTTGTTGAGAGCAACGCTTATTAAGTT 462
Qy 280 ctgagcagtgcaagtggaaggtctccacaggtgfatiaacttggacacatgtggaatat 339
Db 463 CTTCAGAGTGGGTT---GGCATCCCGACATAGGAGTGTGTCAGAGAAAGACATAC 519
Qy 340 aatgcatagtgctgagctccttgccctagcttggagagactgttgacctgtgac 399
Db 520 AATTAAGTACGATGATCTTCTGAGCCTAGCCTCGAAGACCTTCAATTTGTGTCA 579
Qy 400 cgaacattacttgaagacggtgtaataagaccacacagctgcttcctcgaatgaa 459
Db 580 AGAAGTTCAACAAAGAACTGTAATGTTAGTACCTGACCGAGATCAGTAGAATTGAA 639
Qy 460 taatgacataaagaacatttaccagagatgtaacgaagaacttcctgattg 519
Db 640 TATGTGATACAAAGAAATTTATACAGAGACATTAACCAAGATTAACCTCTATATGGT 699
Qy 520 cgaagaagcaataaagaagacatgataacatataagattgagcagcaagaa 579
Db 700 ATTGGGGCTCACTGTAATAG-----TTATCTTATTTGATTTGGTTGGCCAAAAG 753
Qy 580 tacattgaccccgaaacaaacacatacattatagggagacaaagttaactgga 639
Db 754 TACAGAGCAACAGAGCAACAGCAACATACCATACAGAGAAATAAACCTCAGTGGC 813
Qy 640 actgcaagataatgctatcaacacgcatcttgcaagaagacccggaagatgat 699
Db 814 ACTGCCGATATGCTACATCAATGACATCTTGTAATGAGAGATCGCCGAGATGAC 873
Qy 700 ttggaagccctgaagcacaatgatacttcttgcagagcagccctcctgcaagaa 759
Db 874 ATGGAATCATATTAGATATGTTTATGATGATTTATTAAGAACCAACCTGCGATGGCAGG 933
Qy 760 ctcaagcctgacacataaagaagagatatacaaaaatltgtgacacaaagaataact 819

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Db 934 CTAAGGCTGCACACAAAGAAATATGAAAGATTAGTAAGAGATGTCCACG 993
Oy 820 cccattgaagctcctctgtgagaaacttccagagagatggcaacctcgcataatg 879
Db 994 CCTGTGAAGTATTATGTAAGGGGTTTCTCGCAGAAATTGCGATGTACTTAACATAATGT 1053
Oy 880 aggcgactggaacttcttgaanaaaacctgataatgatttlaaggaacctcttcaagac 939
Db 1054 CGTGGCTACGCTTTGAGGAAGCCCGAGATTACATGTATCTGAGGAGCTATTCCGCAAT 1113
Oy 940 ctcttgaanaaagaagctacacaccttgactatgcctatgatgg 984
Db 1114 CTTTCAGGACCCCTGAACCATCAATATGACTACACATTGATTGG 1158

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Search completed: August 17, 2002, 21:27:32
 Job time: 3856 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 17, 2002, 20:18:06 ; Search time 1693.47 Seconds
(without alignments)
10113.929 Million cell updates/sec

Title: US-09-765-068-1

Perfect score: 1269
Sequence: 1 atgagcattccctcagtagga.....ctgcacagcgcacaaagta 1269

Scoring table: IDENTITY_NDC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 674847542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estda:*
2: em_estda:*
3: em_estln:*
4: em_estln:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hlc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	615.4	48.5	930	10	BF308810 601889729
2	599	47.2	935	9	AL524795
3	560	44.1	940	9	AL526554
4	495.8	39.1	841	10	BE786814 601477624
5	494	38.9	885	10	BI196952 602755974
6	480.8	37.9	594	10	BI390112 602755974
7	471.8	37.2	847	10	BI409005 602966091
8	464.8	36.6	889	10	BM008018 603617763
9	461.4	36.4	776	10	BM007847 603617532
10	435.4	34.3	466	10	W90174
11	434.2	34.2	759	9	AJ394482
12	432	34.0	868	10	BG745206 602723541
13	416.8	32.8	777	10	BM049421 603624023
14	414.2	32.6	553	9	AV614943
15	413.4	32.6	466	9	AA210141
16	413	32.5	844	10	BM048132 603620483
17	403.4	31.8	836	10	BI664914 603290366

18	400.8	31.6	659	9	AL633314
19	386.2	30.4	828	10	BE562448
20	380.8	29.9	688	10	BI739265
21	379.4	29.9	727	10	BG260877
22	379.4	29.9	962	10	BF980670
23	375.4	29.6	826	10	BM048049
24	368.8	29.1	861	10	BG398668
25	367.2	28.9	613	10	BE793767
26	366.6	28.9	819	10	BI104367
27	366.4	28.9	906	10	BF160061
28	364.6	28.7	656	9	AW990004
29	364.2	28.7	885	10	BG387674
30	361.8	28.5	637	10	BF141805
31	354	27.9	716	10	BG249775
32	352.8	27.8	527	9	AW652323
33	350.6	27.6	691	9	AW127769
34	347.4	27.4	706	10	BE374102
35	347	27.3	715	10	BE732523
36	346.8	27.3	821	10	BI085586
37	346.2	27.3	648	10	BG335875
38	344.2	27.1	373	9	AA210142
39	344.2	27.1	812	10	BG740368
40	343.4	27.1	838	10	BI911256
41	341.2	26.9	845	9	AL558268
42	339.8	26.9	1041	10	BF237650
43	339.6	26.8	575	10	BG085938
44	339.4	26.7	878	10	BE900116
45	336.6	26.5	842	9	AI892993

ALIGNMENTS

RESULT 1
LOCUS BF308810 930 bp mRNA linear EST 21-NOV-2000
DEFINITION 601889729F1 NIH_MGC_17 Homo sapiens CDNA clone IMAGE:413494 5',
LOCUS mRNA sequence.
ACCESSION BF308810 GI:11256075
VERSION BF308810
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE NIH-MGC http://mgc.nci.nih.gov/
1 (bases 1 to 930)
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgapds@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at: Image.lnl.gov
Plate: LNCM1008 row: j column: 07
High quality sequence stop: 684.
location/Qualifiers
1. 930
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4123494"
/clone_id="NIH_MGC_17"
/issue_type="rhabdomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/note="organ: muscle; vector: pORF7; site_1: EcoRI;
site_2: XhoI; cDNA made by oligo-dT priming.
directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCAAGAG(G). size-selected >500bp
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald W. Rubin (University

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source

of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
 BASE COUNT 261 a 223 c 236 g 210 t
 ORIGIN

Query Match 48.5%; Score 615.4; DB 10; Length 930;
 Best Local Similarity 97.9%; Pred. No. 4.3e-159;
 Matches 698; Conservative 0; Mismatches 6; Indels 9; Gaps 7;

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Oy 72 ctgctctgacacatctgtgctctctatcgctccctggtgttctatgtgtggaacccatt 131
Db 2 ctgctctgacacatctgtgctctctatcgctccctggtgttctatgtgtggaacccatt 61
Oy 132 cagggttggcagaagatagatgtgtggaacttcggaagctcagattagtaaaatct 191
Db 62 cagggttggcagaagatagatgtgtggaacttcggaagctcagattagtaaaatct 121
Oy 132 ctacacatgatataatgtatgaataaactggaacccaataataacgtgtctccacagt 251
Db 132 ctacacatgatataatgtatgaataaactggaacccaataataacgtgtctccacagt 181
Oy 252 tcaattagaatcacatattataaacagcttgagcagtgagtgagtgagtgagtgagtg 311
Db 182 tcaattagaatcacatattataaacagcttgagcagtgagtgagtgagtgagtgagtg 241
Oy 312 gtattacttggacacatgtggaataatataatgcatgtgtgtgagcttctgtgacctag 371
Db 242 gtattacttggacacatgtggaataatataatgcatgtgtgtgagcttctgtgacctag 301
Oy 372 ctgtgaggaactgtgtgacctctgtgacctggaacatttacttgaagagtggttattatg 431
Db 302 ctgtgaggaactgtgtgacctctgtgacctggaacatttacttgaagagtggttattatg 361
Oy 432 agccatccagctgtctctcgaatgaaatgacgtgacccaagaacccattaccagaga 491
Db 362 agccatccagctgtctctcgaatgaaatgacgtgacccaagaacccattaccagaga 421
Oy 492 tgcgaagccagaagaactctctgtgtgtgcgaagcaatgaagaagacatgttatata 551
Db 422 tgcgaagccagaagaactctctgtgtgtgcgaagcaatgaagaagacatgttatata 481
Oy 552 catatagaacttggacgtggtggaagaatgacatgaccccggaacccaataaacatcac 611
Db 482 catatagaacttggacgtggtggaagaatgacatgaccccggaacccaataaacatcac 539
Oy 612 ttatagggaacacaagaatttaactggaactgcaagatatgtctatcaacagcatct 671
Db 540 ttatagggaacacaagaatttaactggaactgcaagatatgtctatcaacagcatct 598
Oy 672 tggcagaagacagaagccggaagatgatttggaaagccctaggccatatgttattt 731
Db 599 tggcagaagacagaagccggaagatgatttggaaagccctaggccatatgttattt 656
Oy 732 ccttggaagcagcctccctggaagagctcaagctgacacataataaagaaga 784
Db 657 ccttggaagcagcctccctggaagagctcaagctgacacataataaagaaga 705

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RESULT 2
 AL524795 935 bp mRNA linear EST 13-FEB-2001
 LOCUS AL524795 LTI.NFL003.NBC3 Homo sapiens cDNA clone CS0DC008Y123 5
 DEFINITION prime, mRNA sequence.
 ACCESSION AL524795
 VERSION AL524795.1 GI:12788288
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 REFERENCE 1 (bases 1 to 935)
 AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polayes, D.

TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT Contact: genoscope

Genoscope - Centre National de Sequencage
 BP 191 91006 Evry cedex - France
 Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES
 Source location/Qualifiers

1..935
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="CS0DC008Y123"
 /clone_11b="LTI.NFL003.NBC3"
 /sex="male"
 /tissue_type="neuroblastoma cells"
 /lab_host="DH10B"
 /note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by life technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@life.com URL : http://fulllength.invitrogen.com"
 BASE COUNT 247 a 235 c 231 g 220 t 2 others
 ORIGIN

Query Match 47.2%; Score 599; DB 9; Length 935;
 Best Local Similarity 100.0%; Pred. No. 1.5e-154;
 Matches 599; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Oy 671 ttggcagaagagaagccggaagatgatttggaaagccctaggccatatgttcatgtatt 730
Db 1 ttggcagaagagaagccggaagatgatttggaaagccctaggccatatgttcatgtatt 60
Oy 731 tccctcgagcagcctccctctggaagagctaaagctgacacattaaagagagatatt 790
Db 61 tccctcgagcagcctccctctggaagagctaaagctgacacattaaagagagatatt 120
Oy 791 aaaaaattggtgacacccaagaagaatctccattggaagctctctgtggaactttccag 850
Db 121 aaaaaattggtgacacccaagaagaatctccattggaagctctctgtggaactttccag 180
Oy 851 aggaagatgcaacactctctcgataltgcaagcgagctggaacttcttgaaaaacctgatt 910
Db 181 aggaagatgcaacactctctcgataltgcaagcgagctggaacttcttgaaaaacctgatt 240
Oy 911 atgagatattacgagacctcttcacagaccttcttgaagaagaagcttcaacaccttgaat 970
Db 241 atgagatattacgagacctcttcacagaccttcttgaagaagaagcttcaacaccttgaat 300
Oy 971 atgctatgattgggttgggaagaccttcttcaacagctgagtgagtgagtgagtgagtg 1030
Db 301 atgctatgattgggttgggaagaccttcttcaacagctgagtgagtgagtgagtgagtg 360
Oy 1031 ctgtgcatctgcaataactcgagaagccacacacataaggaatgcgcacatcaacagc 1090
Db 361 ctgtgcatctgcaataactcgagaagccacacacataaggaatgcgcacatcaacagc 420
Oy 1091 agcctctcgaaataagtggtttagctcaacaaatggagagtgagtgagtgagtgagtg 1150
Db 421 agcctctcgaaataagtggtttagctcaacaaatggagagtgagtgagtgagtgagtg 480
Oy 1151 cggagagccacatccacatcaacacacagctcagtcggaagtgagtgagtgagtgagtg 1210
Db 481 cggagagccacatccacatcaacacacagctcagtcggaagtgagtgagtgagtgagtg 540
Oy 1211 ctaagtgtcgtgttctttaaaggaaaggaagactgtctcagcgcaacagtga 1269
Db 541 ctaagtgtcgtgttctttaaaggaaaggaagactgtctcagcgcaacagtga 599

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RESULT 3
AL526554 940 bp mRNA linear EST 13-FEB-2001
LOCUS AL526554 LNL_NFL003.NBC3 Homo sapiens cDNA clone CS0DC014YF07 5
DEFINITION prime, mRNA sequence.
ACCESSION AL526554
VERSION AL526554.1 GI:12790047
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 940)
AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
1. 940
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DC014YF07"
/clone_1ib="LNL_NFL003.NBC3"
/sex="male"
/tissue.type="neuroblastoma cells"
/lab.host="DH10B"
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed
by Life Technologies. Contact: Feng Liang Life
Technologies, a division of Invitrogen 9800 Medical Center
Drive Rockville, Maryland 20850, USA Fax : (1) 301 610
8371 Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"

BASE COUNT 244 a 248 c 222 g 226 t

Query Match 44.1%; Score 560; DB 9; Length 940;
Best Local Similarity 100.0%; Pred. No. 9.1e-144;
Matches 560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 361 GGCATCGCCATCATACACACAGCCTCTTGAATACAGTGTTAGTCAACCAATGAG 420
QY 1130 agctgaatgttgatgatccacgagagccactccaatcacaatcagctcgcg 1189
DB 421 AGCTGAATGTTGATGATCCACGAGGAGCCACCTCATATGCACCAATACAGCTCATCCG 480
QY 1190 aggttgaggttagtgaggaagcctaagtcgtcgttcttctaagaggaaggaaga 1249
DB 481 AGCTGAGGCTAGTGGAGGAAGCTAAGTGTCTGTTCTTTAAGAGAAAAAGAAAGA 540
QY 1250 ctgctcagcgccacaagtga 1269
DB 541 CTGCTCAGCCGACCACTGA 560

RESULT 4
BE766814 841 bp mRNA linear EST 20-OCT-2000
LOCUS BE766814
DEFINITION 601477624F1 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:3880565 5',
RNA sequence.
ACCESSION BE766814
VERSION BE766814.1 GI:10208012
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 841)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: DCTD/DRP/Gazdar
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LMA9647 row: p column: 06
High quality sequence stop: 551.
Location/Qualifiers
1. 841
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3880565"
/clone_1ib="NIH_MGC_68"
/tissue.type="large cell carcinoma"
/lab.host="DH10B (phage-resistant)"
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.8 kb. Library constructed by Life
Technologies."

BASE COUNT 257 a 210 c 212 g 162 t

Query Match 39.1%; Score 495.8; DB 10; Length 841;
Best Local Similarity 94.7%; Pred. No. 5e-126;
Matches 567; Conservative 0; Mismatches 27; Indels 5; Gaps 5;
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Library Gallus gallus cDNA clone ppgic-pk03.d8.5' similar to
 g111545751 ref|NP_071331.1| casein kinase 1, gamma 1 [Homo sapiens
], mRNA sequence.
 1 dbj|BAB17838.1| (AB042562) casein kinase 1 gamma 1 [Homo sapiens
], mRNA sequence.
 BI390112
 BI390112.1 GI:15083394
 EST.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

Chicken.
 Gallus gallus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 Phasianinae; Gallus.

REFERENCE
 1 (bases 1 to 594)
 Porter, T.E. and Cogburn, L.A.
 ESTs from Primary Chicken Pituitary/Hypothalamus/Pineal cDNA
 Library USDA/IRAFs Animal Genome Project
 Unpublished (2001)
 CONTACT: Larry A. Cogburn
 University of Delaware
 Townsend Hall, Newark, DE 19717, USA
 Tel: 302-831-1335
 Fax: 302-831-2822
 Email: cogburnudel.edu, www.chickest.udel.edu.

FEATURES
 source
 1..594
 /organism="Gallus gallus"
 /strain="Commercial broiler chicken"
 /db_xref="taxon:9031"
 /clone="ppgic-pk03.d8"
 /clone_lib="Primary Chicken Pituitary/Hypothalamus/Pineal
 library"
 /sex="Male and Female"
 /tissue="Pituitary Gland/Hypothalamus/Pineal Gland"
 /dev_stage="Embryonic (d12,d14,d19); post-hatch (w1,w3,w5
 ,w7,w9)"
 /lab_host="E. coli EM8DH108"
 /note="Vector: PCMVSPORT6. Library made from equivalent
 pools of total RNA isolated from each tissue at different
 ages. Single pass sequencing from 5'-end"
 185 a 145 c 128 g 131 t

BASE COUNT
 ORIGIN

Query Match 37.9%; Score 480.8; DB 10; Length 594;
 Best Local Similarity 87.9%; Pred. No. 6e-122;
 Matches 521; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

184 aaaaatctcaacccaatgatatgtgagcaatcaaaactggaacccaataaaatcacgtgct 243
 Db 2 AAAAATCTTACACCAATGAAATGATGCAATGCAAACTGGAACCAATAAATCAGTCA 61
 QY 244 ccacagctcaattagagtagacagatttataaacagcttgccagtggaagtctc 303
 Db 62 CCACAACTCATTTAGAAATACAGATTTTACAAACAGCTGGAAGTGGCGCTGAAGGCTT 121
 QY 304 ccacagtgatcaacttgtagcaatgtgggaataataatcagtgctgagagctctc 363
 Db 122 CCACAGGTTTATTAATTGACGCTGGGGAAGTACAAACGCAATGGGAGCTGCTT 181
 QY 364 ggccttgctgagagagctgttgtagctgtgagccgaacatttacttggaagagctg 423
 Db 182 GGTCTTACCTTGAAGACCTGTCGACCTCTGCAACAGACGTTCACTCTGAANAACGTA 241
 QY 424 ttaatgtagcaccacagctgcttctcgaaatggaatagctgtagactaaagaacctcat 483
 Db 242 TTAATGATACCAATCCAGTGAATCTCGAATGGAATACGTGATGGAAGAACCTCATC 301
 QY 484 taaccagatgtcaagccagagaactctcgtatggtcgacagaagccaataagaagatc 543
 Db 302 TACCGAATGTCAAGCCAGAAATCTCTTATGCGCGGCAAGGCAATAGAAAGACAC 361
 QY 544 gtataaaccttagaacttgagactggcagaagaatatacccccgaacaaaanaa 603

Db 362 GTCATTCACATCATAGACTTTGGAGCTGGCAGAGAGTACATTTGACCCAGAAACCAAAAA 421
 QY 604 cacataactataggggaacacaaagttaacttgtaactcgaatatatgctataaac 663
 Db 422 CACATACCTTACAGGAGCAACAAAGAGCTTAACCTGGAACGGGAGATACATGTCATCAAC 481
 QY 664 accgacttggaagaagcgaagccgagagatgatttggaagcccgagccatcttc 723
 Db 482 ACCGATCTTGCCANAGCAAAAGTCGTCGAGATACCTTGGAGCCCTTGGCCACATGTT 541
 QY 724 atgatcttcctcgaggcagcctccctggcgaaggaactcaagctgacacat 776
 Db 542 ATGATTTCTCCGAGACAGACTGCTGCGAAGAGCTGANNNTGACACTT 594

RESULT 7
 BI409005 847 bp mRNA linear EST 14-AUG-2001
 LOCUS 602966091F1 NCI_CGAP_Lu33 Mus musculus cDNA clone IMAGE:5121407 5',
 DEFINITION
 mRNA sequence.
 ACCESSION BI409005
 VERSION BI409005.1 GI:15169928
 KEYWORDS
 SOURCE EST.
 ORGANISM house mouse.
 Mus musculus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 847)
 NIH-MGC <http://mgc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cgapds.rem@nih.gov
 Tissue Procurement: Gilbert Smith, Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
 Bonaldo, Ph.D.
 cDNA library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>
 Plate: LHAM1296 row: e column: 24
 High quality sequence start: 7
 High quality sequence stop: 846.
 Location/Qualifiers
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 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="IMAGE:5121407"
 /clone_lib="NCI-CGAP_Lu33"
 /tissue="pooled lung tumors"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: Lung; Vector: pTZ19D-pac (Pharmacia) with a
 modified polylinker. Site 1: NotI; Site 2: EcoRI; 1st
 strand cDNA was prepared from mRNA obtained from pooled
 lung tumors with a NotI - oligo(dT) primer [5'
 TGTACCAATCTGAGAGTGGAGGGCGGCTGTGTTTATTTT 3']
 Double-stranded cDNA was ligated to Eco RI adaptors
 (Pharmacia), digested with NotI and cloned into the Not
 I and Eco RI sites of the modified pTZ19D vector. Library
 went through one round of normalization, and was
 constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT
 ORIGIN

Query Match 37.2%; Score 471.8; DB 10; Length 847;
 Best Local Similarity 74.9%; Pred. No. 2.2e-119;
 Matches 631; Conservative 0; Mismatches 207; Indels 5; Gaps 3;

143 agaagatagatgtggaacttgagagctcagattaggtaaatctacacaat 202

Db 9 AGAAGATGAGCTGTGGGAACTTCGGGGAGCTTCGCCCTAGGAAAGAAATCTGATACAAATG 68
Qy 203 aatagttagcaatcaaatggaacccaataaatacaagtgtccacagcttcattagagt 262
Db 69 AGTAGTGGCTATCAAGTGTGAGCCCATCAAGTCCCGGGCCCAACAGCTGCACCTGGAGT 128
Qy 263 acaagattataaagactgtgagtgagtgagtgagtgagtgagtgagtgagtgagtgagtg 322
Db 129 ACCGCTTTTACAGACGCTACAGACGACGACGACGACGACGACGACGACGACGACGACG 185
Qy 323 gacatgtggaagaataataataataataataataataataataataataataataataata 382
Db 186 GCGCTTGTGGAGATACACGACGACGACGACGACGACGACGACGACGACGACGACGACG 245
Qy 383 tttttagcctctgtgacccaatttactttgaagaacggtgttaataatgaatgaatgaatga 442
Db 246 TTTTGGACCTGTGGACCGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 305
Qy 443 tgccttctgcaatggaatgagtgcaactcaagaacactcaattacccagagatgcaagcag 502
Db 306 TGATCACCGCATGAGTACGACGACGACGACGACGACGACGACGACGACGACGACGACG 365
Qy 503 agaatctctgattgtgtgcaagaagaataagaagaagaagaagaagaagaagaagaagaaga 562
Db 366 AGAATCTCTGTGGTGGGCG 425
Qy 563 ttgagctgtgcaagaagaatatactgaccccgaaacccaacaaacacatactataagagac 622
Db 426 TTGGGCTGGCCAGAGAGTACATCCCTGAGACTTAAGACACATCCCATATATGCGGAGC 485
Qy 623 acaaaagttaactggaactgcaagaatatactatctatacaacagcactcttgcaagaagc 682
Db 486 ACAAGAGCTGACACAGGCACTCGCGCTACATGAGCATCAACAGCACTTGGGCAAAAGAGC 545
Qy 683 aaaaacggaagaagatttggaagccctgagccatgatttatttcttcttcttcttcttct 742
Db 546 AGAGCGCGCGGATGACTGAGGCGCGCTGAGACACATCTTATGACTTCTGCGCGGCA 605
Qy 743 gctccctctgcaagaagactcaagagctgacac-attaaagaagataatcaaaaattgct 801
Db 606 GTTGCCCTGTGCGAGGCGCTGAAGGAGACGACGCTGAAGGCGCTGAAGGCGCTGAAGG 665
Qy 802 gaacccaagaagaataactcccatggaagctctctgtggaacttccagaagaagatgga 861
Db 666 GACACCAAGCGCTGACACACACATCGAGGTGCTGTGAGACTTCCCGAGAGAGTGGCC 725
Qy 862 accaaccttgatatactgtaggcagactggaactcttcttgaaaaacactgattatatta 921
Db 726 ACCTATTGGCGCTATGTCGGCGCTGACATTTTGTGAAGCCAGACTTACGACTACCTG 785
Qy 922 cgaacccctctcaagaacactcttgaagaagaagaagctacacacttgaactatgctatgat 981
Db 786 AGGAGAGCTTCTACAGTACCTTTTG-ACCGAGCGGCTACGTTGTGACTTACAGATATAC 844
Qy 982 tgg 984
Db 845 TGG 847

RESULT 8
LOCUS BM008018 889 bp mRNA linear EST 30-OCT-2001
DEFINITION 603617763F1 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:5451062 5',
mRNA sequence.
ACCESSION BM008018
VERSION BM008018.1 GI:16522372
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 889)
AUTHORS NIH-MGC <http://mgc.ncl.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>
plate: LCM1940 row: m column: 15
High quality sequence stop: 857.
Location/Qualifiers
1. 889
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5451062"
/clone_id="NIH_MGC_113"
/lab_host="DH10B (phage-resistant)"
/note="Organ: spleen; Vector: pOMB7; site: 1: XhoI; site: 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGGAG(C). Library constructed by Ling Hong in the
Laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC library."
BASE COUNT 196 a 278 c 277 g 138 t
ORIGIN
Query Match 36.6%; Score 464.8; DB 10; Length 889;
Best Local Similarity 73.9%; Pred. No. 1,9e-117;
Matches 630; Conservative 0; Mismatches 217; Indels 5; Gaps 3;
Qy 89 gctccatgctctctgtgaggttcttatgtgtggaacccaactcaaggtgtgcaagaaga 148
Db 43 GCTGGGAGACCGAGCTCGGGGCTCTGATGGGGCCCCCAACTCGGCTGGCAAGAGA 102
Qy 149 taggatgtggaactctggaagctcagattagtaaaatctctacacaaatgatatg 208
Db 103 TCGGCTGCGGAACTTCGGGAGCTCCGCTAGGAAAGATCTTATCAATTAATACG 162
Qy 209 tagcaatcaaatggaacccaataaataacagtgctcacaagcttcattagatagatagat 268
Db 163 TGGCTATCAATTTGAGAGCGATCAAGTCCCGCGCCGACAGCTCACTGAGATACCGGT 222
Qy 269 ttataacagctgtgcaagtgcaagtgtaaggtctcccaagagtgatattacttggacat 328
Db 223 TCTACAAAGCACT--CAGCGCCACAGAGGCGTCCCTCAAGTCTACTCTGTCGGT 279
Qy 329 gtggaataataatgcaatggtgtgagctctctgtgagcttggagcttggagcttgg 388
Db 280 GCGGGAAGTACAAAGCCATGCTGAGCTGCTGGGGCCAGGCTGAGAGACTGTTCCG 339
Qy 389 acctctgacgaacattacttgaagaagcgtgttaatgataagccatccagctctt 448
Db 340 ACCTGTGGAGACCGGACCTTCACGCTCAAGAGCGGTGATGATGCGCATCGACTGATCA 399
Qy 449 ctggaatggaatagtgactcaagaacactcatttcagagatgttaagcagaagaact 508
Db 400 CGGCGATGAGATATGTGCACCAAGAGCCCTAAATCTTCCGGGAGTGAAGCCCAAGACT 459
Qy 509 tccctgattgtgtgcaagaagcacaagaagaagcagtgtatataacacattatagacttggac 568
Db 460 TCTGTGTGGCGCCCGCGGAGCAAGCGGACGATGCGCATTCACATATGACTGTGGGC 519
Qy 569 tggcgaagaatattgacccgaaacccaacaaacacataccttataagggaacacaaa 628
Db 520 TGGCCAGAGAGTATCATGAGCCCGAGACCAAGACCAATCCCTACCGGAGACACAAAGA 579
Qy 629 gtttaactggaactgcaagaatataatgtctatcaacagcactcttggaagaagaagcc 688

Db	580	GCTTCACCGGACCGCGGCTACATGACATCAACACCGACTCTGGCAAGGACGACACCC	639
Qy	689	ggagagatgatatttggaaagcccttaggcacatgatgtcaatgattcccttcgaaagcagctcc	748
Db	640	GCCGGAGACACTGGTAGGCGCTGGGGCCACAGTTTCATCTACTTCTCTGGCGGACACTTCC	699
Qy	749	ccttgcaagagcttaagctgtcacacatcaaaagagatgataaaaatttgtagcacca	808
Db	700	CCTGGCAGGGGCTCAAGGCGCACACGCTCAAGGACCGGTACCGAGAAAGTCCGGGACACCA	759
Qy	809	aaagaaatactcccatcttgaagctctctgtgtgaagactttccagagagatgtgcaacactac	868
Db	760	AACGGGCCAAGGCCAATCGAGGGGTGCTCTCGAGAAC-TTCCAGAGGAGATGGC-ACGTACC	817
Qy	869	ttcgaatagtcaagcgcagctgactctcttgaaaaacctgatatatgagtatttaagygacc	928
Db	818	TGCGGTATGATGGGGCGGCTTGGACTTCTTCGAGAAAGCCGATTTATACATCAACCTGGCGAAG	877
Qy	929	tcttcacagacc 940	
Db	878	TTTAAACCGACC 889	

RESULT	9
LOCUS	BM007847
DEFINITION	776 bp mRNA linear EST 30-OCT-2001
ACCESSION	60361753F1 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:5450743 5',
VERSION	mRNA sequence.
KEYWORDS	BM007847
SOURCE	BM007847.1 GI:16522201
	EST.
	human.

ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE	1 (bases 1 to 776)
AUTHORS	NIH-MGC http://mgc.ncl.nih.gov/ .
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D.

Email: cgaabbs-r@mail.nih.gov
Tissue procurement: Dr. Mark Watson
cDNA library preparation: Ling Hong/Rubin Laboratory
cDNA library arrayed by: The I.M.A.G.E. Consortium (LMNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LMNL at:
<http://image.jnl.gov>
plates: LMCL1938 row: p column: 08
high quality sequence stop: 772.

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FEATURES
source      location/qualifiers
1. .776

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5450743"
/clone_1lb="NIH_MGC_113"
/lab_host="DH10B (phage-resistant)"
/notice="Organ: spleen; Vector: pOT7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally clone into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

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Query Match 36.4%; Score 461.4; DB 10; Length 776;
Best Local Similarity 75.6%; Pred. No. 1.6e-115;
Matches 586; Conservative 0; Mismatches 186; Indels 3; Gaps 1;

QY	143	agaagatagatgtyggyggaactctggagagccacgattgtaaaatcttaacccaat	202
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OY	203	aatagtagcaatacaactctggaaccaataaaatcacgtgctccaaagcttcaatlaagat	262
Db	62	AATAGTGGCTATCAATTTGATGGCCGATCAAGTCCCGGGCCCCGGAGCTGCACCTGGAGT	121
OY	263	acaaatttataaacaagcttggcagtgcaagtgaaagtcctccacaggtgtataacttgg	322
Db	122	ACCGGTTCTTACAAGACAGCT---CAACGGCCACAGAGGGCGTCCCTCAGGTCTACTACTTCG	178
OY	323	gaccaatggyggaataatataatgcatcagtgycgcggagctcctctggccctagcttgaagagat	382
Db	179	GTCCCTGGGGAGATACACCCGATGGTGTGTGGACTCTGTGGGCCCCAGCTGGGGAGCC	238
OY	383	tgtttgacctctgtgtaccgaacattacttgaagaagcgtgtlaatgtaaccatccagc	442
Db	239	TGTTTGACTCTGTGCCACCGGACCTTCAAGCTCTAAGAGGTGTGATGTGTCGATCCAGC	298
OY	443	tgcttctcgaatggaatacgtgcacccaaagaacctcatctaccagagatgcaagccag	502
Db	299	TGATCACCCGATGAGATGTGTGCACACCAAGAGCCTTATCTACCGGGAGCTGTGAAGCCCG	358
OY	503	agaattctctgattggtgcgaaggaacaaataagaagaagcagtataaacaattatagat	562
Db	359	AGAACTTCTCTGGTGGGCGGCCCGGGGACCAAGGGCAGCACTATGCCATCATCGACT	418
OY	563	ttggaactgccaagaatatacatctgaccccggaacccaanaaacacatacctataaggagac	622
Db	419	TGCGGCTTGCCACGAGATACATCGAACCCGAGCCAAAGACATCCGTAACCGCGAGC	478
OY	623	acaaaagttlaactggaacctgcaagatatatgtctatacaacagcacttggcaaaagc	682
Db	479	ACAAGAGCCTGACGGGGCAGCGGCGCTCATATGAGCATCAACACGCACTGGGCAAGAGC	538
OY	683	aaagccggaagatgattttgaaagccctcagagccatgttatalgtaattcttcgaagca	742
Db	539	AGAGCGCGCCGACACCTGTGAGGGGCTGTGGGCAATATTTCTGTGTTCTCTGCCGGCA	598
OY	743	gcttcctctgcaagagactcaagcctgacacataaaagaagatatacaaaaatctggtg	802
Db	599	GCCTTCCTTGAGGGGGCTCAAGGCGCAAGCCTCAAGAGGGGTATACCAAGAAATCGGGG	658
OY	803	acacccaaaagaaatactcccatctgaagctctctgtgtgaagacttccagaagagatgcaaa	862
Db	659	ACACCAAAAGCGCCACGCCCATCGAGGTGCTCTGCGAAGAACTTCCCAAGAGAGATGGCCA	718
OY	863	cctactctcgatatgtcagaggagcagcagactctttaaanaaacctgatatgaagta	917
Db	719	GTACTCTCGCTATGTGGCGCCCTGGAACTTCTTGAAGAGCGCACTATGACTTA 773	

RESULT	10
W90174	
LOCUS	
DEFINITION	
	W90174 466 bp mRNA linear EST 08-JUL-1996
	zh78b03.i1 Soares-fetal_liver_spleen_ILFSL.S1 Homo sapiens CDNA
	clone IMAGE:418157 5' similar to SW:KCID_RAT Q06486 CASEIN KINASE
	1, DELTA ISOFORM ;, mRNA sequence.

ACCESSION	VERSION
W90174	GI:1406473
W90174.1	

KEYWORDS *est.*
SOURCE *human.*

ORGANISM	Homio sapiens
Eukaryota; Metazoa; Chordata; Granlata; Vertebrata; Euteleostomi;	

REFERENCE
1 (bases 1 to 466)
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

AUTHORS

Hillier, L., Clark, N., Dubouque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Palfrey, D., Phillips, E., Searles, W., Shaw, R., Smith, B., Thompson, E., Watson, C.

KIRKIN, L., KOHLING, I., SOARES, M., JAIN, F., KLEVANSKIS, E.,
R., WILLIAMSON, A., WOHLMANN, P. and WILSON, R.
at: North Walsham, Dorset

THE WASNU-MEICK ESI PROJECT

Db 478 TGGCCAAAGACTACATGACCCCGAGACCAAAAACATCCCTACAGAGACACAAAGA 537
Qy 629 gtttaactggaactcgaagatatagtctatacaacagcatcttggcaagaagaagcc 688
Db 538 GCGTACGAGGGAGCGCGGTACATGAGCATCAACACCCACTCGGAGAGAACAAAGCC 597
Qy 689 ggaagatgatttgaagcccttaagcatatgttcatgtatttcttcgagagccctcc 748
Db 598 GCAGGAGACGACCTGGAAGCGTTGGCCATATGTTTATGTTCTCCCGGAGAGCTTC 657
Qy 749 ccttggcaagactcaagctggaacattaaagagagatctcaaaaatttgtagacca 808
Db 658 CTTGCGAGGGGCTTAAGCGGACACACTCAAGAGAGATACAAAGATCGGGAGACCA 717
Qy 809 aaagaaactaccatctgaagctctctgtgagaacttc 847
Db 718 AAGCAGCCACCGCGGTGAGGTGCTGTGTGAGACTTCC 756

RESULT 12
Bg745206 868 bp mRNA linear EST 15-MAY-2001
LOCUS 602723541F1 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:4849811 5',
DEFINITION mRNA sequence.
ACCESSION Bg745206
VERSION Bg745206.1 GI:14055859
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 868)
AUTHORS NIH-MGC http://mgs.ncl.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabds-remail.nih.gov
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.nih.gov
Plate: L1CM1690 row: a column: 12
High quality sequence stop: 751.
Location/Qualifiers
1. 868
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4849811"
/clone_11D="NIH_MGC_113"
/lab_host="DH10B (phage-resistant)"
/note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
Laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

BASE COUNT 196 a 269 c 276 g 127 t
ORIGIN

Query Match 34.08; Score 432; DB 10; Length 868;
Best Local Similarity 73.38; Pred. No. 2.2e-108;
Matches 608; Conservative 0; Mismatches 215; Indels 7; Gaps 4;

Qy 89 gctctcatctctctctgtggttcttattgtgtggagcccaactcaaggtgtgcaagaaga 148
Db 43 GCTCGGGACCAAGCTCGGGGCTCTGATGATGGGCCCAACTTCGCGCTCGGCAAGAA 102

Qy 149 taggatgtggaactctggagagctcagataggttaaaatctctacacaaatgaatg 208
Db 103 TCGGCTCGCGCAACTCTGGGGAGCTCCGCTAGGAAGAAATCTATCAAAATGAATCG 162
Qy 209 taagaatcaaaactggaaccaaataatcagtgctcccaagcttcaatttaagtagacagat 268
Db 163 TGGCTATCAAAATTTGAGCGCATCAAGTCCGGGGCCCGCAGCTGCATCGAGTACCGGT 222
Qy 269 ttataacagcttggcaagtgcaagtgtaaggtctcccaaggtgtatattcatttggacat 328
Db 223 TCTACAAAGCACT--CAGCGCCACAGAGGCGCTCCCTCAAGGTCTACTACTTCGTTCCGT 279
Qy 329 gtgggaataataatgcatatgtgtgtgagctcccttggccctcagcttggagagattgtt 388
Db 280 GCGGGAAGTACAAAGCGCATGGTGTGAGCTGTGGAGCTGTGGGCCAGAGCTGAGACCTGTTCCG 339
Qy 389 accctgtgacagcaacattccttgaagagcgtgtatgatagacacatccagctgtctt 448
Db 340 ACTGTGCGACCGGACCTTCACGCTCAAGAGAGGTGTATGATCGCATCCAGCTGATCA 399
Qy 449 ctggaatggaatcagtgcaactcaaaagaacctcattaccagatgtcaagccagaagaact 508
Db 400 CGGCATGTGAGTATGTGACACCAAGAGCCTAATCTACCGGAGCGTGAAGCCCGAGAACT 459
Qy 509 tccctgattgtctgaagagcaataagaagagcatgttatcacattataagactttgac 568
Db 460 TCCGTGGTGGCGCCCGCGGGACCAAGCGCGCATGTCCATCTGCACTTCGCTGGGC 519
Qy 569 tggcgaaggaatatactatgaccgcaacaaacaaacacataccttataggagaaacaa 628
Db 520 TGGCCAAAGAGTACATGACGCCCGAGACCAAGAACACATCCGTCAGCGGACAGCAAGA 579
Qy 629 gtttaactggaactcgaagatatagtctatacaacagcatcttggcaagaagaagcc 688
Db 580 GCTGACGAGGCGACGGCGGTACATGAGCATCAACACACACTGCGGCAAGAGAGAGAGCC 639
Qy 689 ggaagatgatttgaagcccttaagcattatgtcatatttcttcttggagagccctcc 748
Db 640 -GCGGAGGACTGTGAAGGCGTGGGCCCATGTATATATCTCTCGCGGACACATC 698
Qy 749 ccttggcaagactcaaggtctacacatlaaagaagagatlatcaaaaatttggtagacca 808
Db 699 CTTGGCAGGGCTCAAGGGCGACACGCTCAACAGAGCGGTACAGAGATCGGGAGACAA 758
Qy 809 aaagaaactaccatctgaagctctctgtgagaacttcagagga-gatggcaacttac 867
Db 759 AACGCGCCACGCGCATCGAGGTCTGTGAGAACTTCCAGAGAGCATGCGACGCTAC 818
Qy 868 cttagatatgcaagcagcttgaacttcttgaaaaacctgtattagatga 917
Db 819 CGGGGCCAAGT--GCGGGCTGACATCTTGAAGAGGCGGAATACGACTA 866

RESULT 13
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LOCUS 603624023F1 NIH_MGC_40 Homo sapiens cDNA clone IMAGE:5449924 5',
DEFINITION mRNA sequence.
ACCESSION BM049421
VERSION BM049421.1 GI:16778688
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 777)
AUTHORS NIH-MGC http://mgs.ncl.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabds-remail.nih.gov
Tissue Procurement: DCTD/DTF


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Db 252 GAATGACTCCATGAACTTCTGTGAAAACTCCAGAGAGATGCAACTACTGCG 311
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QY 873 atatgaagcgaactgactcttcttgaataaacctgattatgaglatctacgacccctt 932
|||||
Db 312 ATATGTCAGCGATTGACTCTTTGAAAAAAGCTGACTATGAGTATTTAGCAGCGCTT 371
|||
QY 933 cacagaccccttcttgaataaagagctacacacttgactatgactatgattgggtggag 992
|||||
Db 372 GACAGACCTCTTTGAAAGGAAAGGCTACACCTTTGACTACNCGTATGATGGGTGGAG 431
|||
QY 993 acctatccacccagtagtgcagf-tcagctagatc-tggtgactgcaataact 1050
|||||
Db 432 GCGTATGCGACCTCCATAGGAGTATGATGATGATGATGATGATGATGATGATGAT 491
|||
QY 1051 cgaagaaagcacaacataagatcgccacacacagagacccctctcgaatacagtg 1110
|||||
Db 492 GGANGAAGCCNCACACACAGGGGTGCGNNCATGACACAGGCTTACGAATAAGAGTG 551
|||
QY 1111 g 1111
|||
Db 552 G 552

RESULT 15
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LOCUS mu42901.r1 Soares_thymus_2NDBT Mus musculus cDNA clone IMAGE:642096
DEFINITION 5' similar to TR:G854737 G854737 CASEIN KINASE 1 GAMMA 3 ISORFORM.
; mRNA sequence.
ACCESSION AA210141
VERSION AA210141.1 GI:1808459
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 466)
REFERENCE 1 (bases 1 to 466)
AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisler,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steppe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
TITLE The WashU-HM Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Marra M/Mouse EST Project
WashU-HM Mouse EST Project
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Tel: 314 286 1800
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Email: mouseest@wustl.edu
This clone is available royalty-free through LBNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:394088
Seq primer: -28m13 rev2 ET from Amersham.
location/Qualifiers
1.466
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/dev_stage="4 weeks"
/lab_host="DH10B"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
polylinker. Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was primed with a Not I - oligo(dT) primer [5',
TGTTCACCAATCTGAGAGCGCGCGCTTTTATTTTATTTTATTTTATTTTATTTTATTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I

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and Eco RI sites of the modified pT73 vector. RNA provided by Dr. Bertrand Jordan. Library went through two rounds of normalization, and was constructed by Bento Soares and M. Fatima Bernaldo."

Query Match 32.6%; Score 413.4; DB 9; Length 466;
Best Local Similarity 94.2%; Pred. No. 2,4e-103;
Matches 440; Conservative 0; Mismatches 26; Indels 1; Gaps 1;

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BASE COUNT 138 a 109 c 103 g 116 t
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